

101042063

GenCore version 5.1.6
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M nucleic - nucleic search, using sw model
run on: October 6, 2003, 09:43:17 ; Search time 4541 Seconds
(without alignments)
16207.095 Million cell updates/sec

itle: US-10-092-063-2
erfect score: 1799
equence: 1 gcgggctgcgcgaacgggt.....cgacgccttccacagtgcga :799

oring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
earched: 2888711 seqs, 2045481386 residues
otal number of hits satisfying chosen parameters: 5777422

inimum DB seq length: 0
aximum DB seq length: 2000000000
ost-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

atabase :

GenEmbl:

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- 2: gb_htg:*
- 3: gb_in:*
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- 33: em_htg_mus:*
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- 36: em_htg_mam:*
- 37: em_htg_vrt:*
- 38: em_sy:*
- 39: em_htgo_hum:*
- 40: em_htgo_mus:*
- 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1794.8	99.8	1799	6	AR181064	AR181064 Sequence
2	1794.8	99.8	1799	6	AR210057	AR210057 Sequence
3	1794.8	99.8	1799	6	AR227867	AR227867 Sequence
4	1794.8	99.8	1799	6	AR244596	AR244596 Sequence
5	1575	87.5	1998	6	AR194794	AR194794 Sequence
6	1575	87.5	1998	9	AF039918	AF039918 Homo sapi
7	1504.2	83.6	2033	9	AF136572	AF136572 Homo sapi
8	1445	80.3	1601	6	AR181083	AR181083 Sequence
9	1445	80.3	1601	6	AR227886	AR227886 Sequence
10	1445	80.3	1601	6	AR244615	AR244615 Sequence
11	1287	71.5	1287	6	AR181065	AR181065 Sequence
12	1287	71.5	1287	6	AR210058	AR210058 Sequence
13	1287	71.5	1287	6	AR227868	AR227868 Sequence
14	1287	71.5	1287	6	AR244597	AR244597 Sequence
15	1286.4	71.5	3157	9	BC020966	BC020966 Homo sapi
16	1277.4	71.0	1287	6	AR181066	AR181066 Sequence
17	1277.4	71.0	1287	6	AR210059	AR210059 Sequence
18	1277.4	71.0	1287	6	AR227869	AR227869 Sequence
19	1277.4	71.0	1287	6	AR244598	AR244598 Sequence
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21	1081.2	60.1	1750	10	AF084569	AF084569 Mesocrice
22	1073	59.6	1633	10	MMU238636	AJ238636 Mus muscu
23	1070.8	59.5	1749	10	AF084568	AF084568 Mesocrice
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25	1063.2	59.1	2099	10	BC015247	BC015247 Mus muscu
26	1051.2	58.4	2119	10	AF006482	AF006482 Mus muscu
27	1049.6	58.3	2119	6	AR194795	AR194795 Sequence
28	342.2	19.0	2693	6	AR181103	AR181103 Sequence
29	342.2	19.0	2693	6	AR244635	AR244635 Sequence
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32	342.2	19.0	2762	6	AR194792	AR194792 Sequence
33	342.2	19.0	2762	6	AR227887	AR227887 Sequence
34	342.2	19.0	2762	6	AR244616	AR244616 Sequence
35	342.2	19.0	2762	6	AR244639	AR244639 Sequence
36	342.2	19.0	2762	9	AF039916	AF039916 Homo sapi
37	340.6	18.9	2670	9	HSM805404	AL834158 Homo sapi
38	340.6	18.9	2693	6	AX591674	AX591674 Sequence
39	340.6	18.9	2736	6	AX364937	AX364937 Sequence
40	340.6	18.9	2765	9	BC025980	BC025980 Homo sapi
41	339	18.8	2564	6	BD127921	BD127921 Primer fo
42	339	18.8	2564	9	AK074691	AK074691 Homo sapi
43	339	18.8	2648	6	AX591676	AX591676 Sequence
44	331.8	18.4	2458	10	RNO277748	AJ277748 Rattus no
45	320.6	17.8	2371	6	AR181101	AR181101 Sequence

ALIGNMENTS

RESULT 1
AR181064
LOCUS AR181064 1799 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 2 from patent US 6335013.
ACCESSION AR181064
VERSION AR181064.1 GI:20223278
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1799)
AUTHORS Ford, J., Mulero, J.J. and Yeung, G.
TITLE Methods and materials relating to CD39-like polypeptides
JOURNAL Patent: US 6335013-A 2 01-JAN-2002;
FEATURES Location/Qualifiers

SOURCE		1. .1799									
SE COUNT		/organism="unknown"									
IGIN		467 a	409 c	472 g	442 t	5	others				
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Best Local Similarity		100.0%; Pred. No. 0;									
Matches 1799; Conservative		0;	Mismatches	0;	Indels	0;	Gaps	0;			
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Q	61	TGTGGAGTGTCTTGGCTGAATCCTCATACAGACAAGATCAATATGGTGTCTGTAGGTTGA	120								
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Q	241	AAAGANTGCCACTTCTTGGGCGACAGTCTTTTTCATCTGCTGGTGTATCCTGTGTTTGA	300								
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Qy	961	CACATAGTTACCTGGGATTTCGATTGAAAGCTGCAAGACTAGCAACCCCTGGAGCCCTGG	1020
Db	961	CACATAGTTACCTGGGATTTCGATTGAAAGCTGCAAGACTAGCAACCCCTGGAGCCCTGG	1020
Qy	1021	AGACAGAAGGACTGATGGGCACACTTTCGGAGTGCCCTGTTTACCGAGATGGTTGGAAG	1080
Db	1021	AGACAGAAGGACTGATGGGCACACTTTCGGAGTGCCCTGTTTACCGAGATGGTTGGAAG	1080
Qy	1081	CAGAGTGGATCTTTGGGGTGTGAAATACCAGTATGGTGGCAACCAAGAAAGGGAGGTGG	1140
Db	1081	CAGAGTGGATCTTTGGGGTGTGAAATACCAGTATGGTGGCAACCAAGAAAGGGAGGTGG	1140
Qy	1141	GCCTTGAGCCCTGCTATGCCGAAGTCTGAGGGTGTGAGGAGGAAACTTCACCCAGCCAG	1200
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Qy	1261	CAGACATGATTGATTATGAAAAGGGGGTATTTTAAAGTTGAAGATTTTGAAGAAAAG	1320
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Db	1501	ACCTGTTGCAGTCTCTGGGATCTCCCATTTGAGGCCACGTACTTCTTGGAGACCTGCAT	1560
Qy	1561	TTGCCAACACCTTTTAAAGGGAGGAGAGAGACACTTAGTCTTGAAGTCTGGGGACA	1620
Db	1561	TTGCCAACACCTTTTAAAGGGAGGAGAGAGACACTTAGTCTTGAAGTCTGGGGACA	1620
Qy	1621	TCCTGGACTTGAGCCTAGAGATTWRGTTAATTAASCGGCCGAGCTTATCCTTWTATRAGT	1680
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AR210057			
LOCUS			
DEFINITION			
Sequence 2 from patent US 6387645.			
ACCESSION			
AR210057			
VERSION			
AR210057.1 GI:21512188			
KEYWORDS			
SOURCE			
ORGANISM			
Unknown.			
Unclassified.			
REFERENCE			
1 (bases 1 to 1799)			
AUTHORS			
Ford, J. and Mulero, J.J.			
TITLE			
Methods and materials relating to novel CD39-like polypeptides			
JOURNAL			
Patent: US 6387645-A 2 14-MAY-2002;			
FEATURES			
Location/Qualifiers			
source			
1. .1799			

AR210057 Sequence 2 from patent US 6387645. linear PAT 20-JUN-2002

RIGIN

Query Match									
Best Local Similarity 99.8%; Score 1794.8; DB 6; Length 1799;									
Matches 1799; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
y	1	CGGGCTGCCGCGCAAGG	TGGCGCGCGCGGCTTTCCTTGTTCCTTGCTCAACAAGAAA	60					
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b	121	AAAAGTGATATAATAA	AGGAACCAAGGAGAAAATTCAGAGGAAAGAAAATTTGCCCTCT	180					
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y	361	GCCCCATCAATGTCA	GCAGCCAGCACCCTTGATGGAAATATGTTGATGCGAGGAGCACTG	420					
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Qy	1021	AGACAGAAAGGACTGAT	GGGCACACCTTCCGGAGTGCCTGTTTACCGAGATGTTTGAAG	1080
Db	1021	AGACAGAAAGGACTGAT	GGGCACACCTTCCGGAGTGCCTGTTTACCGAGATGTTTGAAG	1080
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Db	1081	CAGAGTGGATCTTTGG	GGGTGTGAAATACCAAGTATGGTGGCAACCAAGAAAGGGAGGTGG	1140
Qy	1141	GCCTTGAGCCCTGCTAT	GCCGAAGTGTGAGGGTGGTACGAGGAAACTTCACCAAGCCAG	1200
Db	1141	GCCTTGAGCCCTGCTAT	GCCGAAGTGTGAGGGTGGTACGAGGAAACTTCACCAAGCCAG	1200
Qy	1201	AGGAGTCCAGAGAGGT	TCCCTTCTATGCTTTCTTACTATTATGACCGAGCTGTTGACA	1260
Db	1201	AGGAGTCCAGAGAGGT	TCCCTTCTATGCTTTCTTACTATTATGACCGAGCTGTTGACA	1260
Qy	1261	CAGACATGATTGATTAT	GAAAGGGGGGTATTTTAAAGTTGAAGATTTTGAAGAAAG	1320
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Qy	1321	CCAGGGAAGTGTGTATA	AACTTGGAAACTTCACCTCAGGCAGTCCCTTCTGTGCAATGG	1380
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Qy	1621	TCTGGAATTTGAGCT	TAGAGATTWRGTTAAATTAASCGGCCGAGCTTATCCTTWTATRAGGT	1680
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Qy	1681	AATTTACTTGTGCTG	CGCGTTCACACGTCGTGATGAGGAAACCTGCGTCCCAACTAACGC	1740
Db	1681	AATTTACTTGTGCTG	CGCGTTCACACGTCGTGATGAGGAAACCTGCGTCCCAACTAACGC	1740
Qy	1741	TTGASAMATCCCCTTC	GAGCTGCGATACCAAAAGCCGACGCGCTTCCACAGTGCCA	1799
Db	1741	TTGASAMATCCCCTTC	GAGCTGCGATACCAAAAGCCGACGCGCTTCCACAGTGCCA	1799
RESULT 5				
AR194794				
LOCUS	AR194794	1998 bp	DNA	linear
DEFINITION	Sequence 5 from patent US 6350447.			
ACCESSION	AR194794			
VERSION	AR194794.1 GI:20244231			
KEYWORDS	Unknown.			
SOURCE	Unknown.			
ORGANISM	Unclassified.			
REFERENCE	1 (bases 1 to 1998)			
AUTHORS	Chadwick, B. Paul, and Frischauf, A.-M.			
TITLE	Methods and compositions relating to CD39-like polypeptides and nucleic acids			
JOURNAL	Patent: US 6350447-A 5 26-FEB-2002;			
FEATURES	Location/Qualifiers			
source	1..1998			
BASE COUNT	557 a	449 c	491 g	501 t

ORIGIN

Query Match		97.5%;	Score 1575;	DB 6;	Length 1998;
Best Local Similarity		98.2%;	Pred. No. 0;		
Matches 1620;		Conservative	2;	Mismatches	2;
				Indels	25;
				Gaps	2;
2Y	24	GCGCGCGGTTTTCCTTGGTTCAGTCAAAAGAAATGTGGAGTGTCTTGGCTGAATCC	83		
Db	1	GCGCGCGGTTTTCCTTGGTTCAGTCAAAAGAAATGTGGAGTGTCTTGGCTGAATCC	60		
2Y	84	TCATACAGACAAGATCATTATGGTGCTGT-----AGGTTG	119		
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2Y	120	AAAAAGTGATATAATAAGGAACCAAGGAGAAATTCAGAGGAAAGAAATTCGCTC	179		
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2Y	180	TGCAGGTGTGGAGCAGGATTGCTTCTGCAACAAAGCCCTCCACCCAGCCACATCTTGG	239		
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2Y	240	AAAAGATGGCCACTTCTTGGGGCACAGTCTTTTTCATGCTGGTGGTATCTCCTGTGTTGC	299		
Db	241	AAAAGATGGCCACTTCTTGGGGCACAGTCTTTTTCATGCTGGTGGTATCTCCTGTGTTGC	300		
2Y	300	AGCGTGTCTCCACAGGAACCAAGGACTTGGTTTGAGGGTATCTTCCCTGTCTCCATG	359		
Db	301	AGCGTGTCTCCACAGGAACCAAGGACTTGGTTTGAGGGTATCTTCCCTGTCTCCATG	360		
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b	361	TGCCCCATCAATGTCAAGCCAGCACTTGTATGGAATTAATGTTGATGCAGGAGCACT	420		
Y	420	GGAACTCGAATTCATGTTTACACCTTTGTGCAGAAATGCGAGGAGACTTCCAAATCTA	479		
b	421	GGAACTCGAATTCATGTTTACACCTTTGTGCAGAAATGCGAGGAGACTTCCAAATCTA	480		
Y	480	GAAGGGGAAGTTTGTATTCTGTGAAGCCAGGACTTCTGCTTTTGTAGATCAACCTAAG	539		
b	481	GAAGGGGAAGTTTGTATTCTGTGAAGCCAGGACTTCTGCTTTTGTAGATCAACCTAAG	540		
Y	540	CAGGGTGTGAGACCGTTCAAGGGCTTTAGAGGTGCGCAAGACTCAATCCCCCGAAGT	593		
b	541	CAGGGTGTGAGACCGTTCAAGGGCTTTAGAGGTGCGCAAGACTCAATCCCCCGAAGT	600		
Y	600	CACCTGGAAGAACCCCGAGTGGTCTTAAAGGCACAGCAGGACTACGCTTACTGCCAGAA	659		
b	601	CACCTGGAAGAACCCCGAGTGGTCTTAAAGGCACAGCAGGACTACGCTTACTGCCAGAA	660		
Y	660	CACAAAGCCAGGCTCTGCTCTTTAGGTAAAGGAGATCTTCAGGAAGTCACCTTTCCTG	719		
b	661	CACAAAGCCAGGCTCTGCTCTTTAGGTAAAGGAGATCTTCAGGAAGTCACCTTTCCTG	720		
Y	720	GTACCAAAAGGGCAGTGTAGCATCATGGATCCGACGAGAGGCATATTAGCTTGGGT	779		
b	721	GTACCAAAAGGGCAGTGTAGCATCATGGATCCGACGAGAGGCATATTAGCTTGGGT	780		
Y	780	ACTGTGAATTTCTGACAGGTCAGTGTGATGGCCACAGACAGGAGACTGTGGGACCTTG	839		
b	781	ACTGTGAATTTCTGACAGGTCAGTGTGATGGCCACAGACAGGAGACTGTGGGACCTTG	840		
Y	840	GACCTAGGGGAGGCTCCACCCAAATCAGCTTCTGCTCCCGAGTTTGAGAAATCTGGAA	899		
b	841	GACCTAGGGGAGGCTCCACCCAAATCAGCTTCTGCTCCCGAGTTTGAGAAATCTGGAA	900		
Y	900	CAAACTCCTAGGGCTACCTCAGTCTTCTGAGATGTTTAAACAGCAGCTTATAAGCTCTAT	959		
b	901	CAAACTCCTAGGGCTACCTCAGTCTTCTGAGATGTTTAAACAGCAGCTTATAAGCTCTAT	960		
Y	960	ACACATAGTTTACTCTGGGATTTGGATTGAAAGCTGCAAGACTAGCAACCCCTGGAGCCCTG	1019		
b	961	ACACATAGTTTACTCTGGGATTTGGATTGAAAGCTGCAAGACTAGCAACCCCTGGAGCCCTG	1020		

QY	1020	GAGACAGAAGGACTGATGGGCACACTTTCCGGAGTGCCTGTTTACCGAGATGGTTGGAA	1079
Db	1021	GAGACAGAAGGACTGATGGGCACACTTTCCGGAGTGCCTGTTTACCGAGATGGTTGGAA	1080
QY	1080	GCAGAGTGGATCTTTGGGGGTGTGAAATACCACTATGGTGGCAACCAAGAGGGAGGTG	1139
Db	1081	GCAGAGTGGATCTTTGGGGGTGTGAAATACCACTATGGTGGCAACCAAGAGGGAGGTG	1140
QY	1140	GGCTTTGAGCCCTGCTATGCCGAAGTGCTGAGGGTGTACGAGGAAACCTTACCAGCCCA	1199
Db	1141	GGCTTTGAGCCCTGCTATGCCGAAGTGCTGAGGGTGTACGAGGAAACCTTACCAGCCCA	1200
QY	1200	GAGAGGTCCAGAGAGGTTCTTCTCTATGCTTTCTTCTACTATTATGACCGAGCTGTTGAC	1259
Db	1201	GAGAGGTCCAGAGAGGTTCTTCTCTATGCTTTCTTCTACTATTATGACCGAGCTGTTGAC	1260
QY	1260	ACAGACATGATTGATTATGAAAGGGGGGTATTTTAAAGTTGAAGATTTTGAAGAAAAA	1319
Db	1261	ACAGACATGATTGATTATGAAAGGGGGGTATTTTAAAGTTGAAGATTTTGAAGAAAAA	1320
QY	1320	GCCAGGAAAGTGTGTATTAACCTTGGAAAAACCTCACCTCAGGCAGTCCCTTCTGTGTCATG	1379
Db	1321	GCCAGGAAAGTGTGTATTAACCTTGGAAAAACCTCACCTCAGGCAGTCCCTTCTGTGTCATG	1380
QY	1380	GATCTCAGCTACATCACAGCCCTGTTAAAGGATGSGCTTTGGCTTTGCAGACAGACAGTC	1439
Db	1381	GATCTCAGCTACATCACAGCCCTGTTAAAGGATGSGCTTTGGCTTTGCAGACAGACAGTC	1440
QY	1440	TTCAGCTCACAAAGAAAGTGAAACATAGAGACGGGCTGGGCCCTTGGGGGCCACCTTT	1499
Db	1441	TTCAGCTCACAAAGAAAGTGAAACATAGAGACGGGCTGGGCCCTTGGGGGCCACCTTT	1500
QY	1500	CACCTGTGTCAGTCTCTGGGCATCTCCCATTTAGGGCCACCTACTTCTTGSAGACCTGCA	1559
Db	1501	CACCTGTGTCAGTCTCTGGGCATCTCCCATTTAGGGCCACCTACTTCTTGSAGACCTGCA	1560
QY	1560	TTTGCCAAACACCTTTTAAAGGGAGGAGAGACACTTAGTTTCTGAACCTAGTCTGGGGAC	1619
Db	1561	TTTGCCAAACACCTTTTAAAGGGAGGAGAGACACTTAGTTTCTGAACCTAGTCTGGGAC	1619
QY	1620	ATCCTGGACTTGAGCCTTAGAGATTTMRGTT	1648
Db	1620	ATCCTGGACTTGAGCCTTAGAGATTTAGGT	1648

RESULT 6	AF039918	Homo sapiens	CD39L4	(CD39L4)	mRNA	linear	PRI 21-JUL-1998
LOCUS	AF039918	Homo sapiens	CD39L4	(CD39L4)	mRNA	complete cds.	
DEFINITION	AF039918	Homo sapiens	CD39L4	(CD39L4)	mRNA	complete cds.	
ACCESSION	AF039918	Homo sapiens	CD39L4	(CD39L4)	mRNA	complete cds.	
VERSION	AF039918.1	GI:3335101					
KEYWORDS							
SOURCE		Homo sapiens (human)					
ORGANISM		Homo sapiens					
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
REFERENCE		1 (bases 1 to 1998)					
AUTHORS		Chadwick,B.P., Williamson,J., Sheer,D. and Frischauf,A.-M.					
TITLE		cDNA cloning and chromosomal mapping of a mouse gene with homology to NTPases					
JOURNAL		Mamm. Genome (1997) In press					
REFERENCE		2 (bases 1 to 1998)					
AUTHORS		Chadwick,B.P. and Frischauf,A.M.					
TITLE		The CD39-like gene family: identification of three new human members (CD39L2, CD39L3, and CD39L4), their murine homologues, and a member of the gene family from Drosophila melanogaster					
JOURNAL		Genomics 50 (3), 357-367 (1998)					
MEDLINE		98341119					
PUBMED		9676430					
REFERENCE		3 (bases 1 to 1998)					
AUTHORS		Chadwick,B.P. and Frischauf,A.-M.					
TITLE		Direct Submission					

1472 GACGGGCTGGGCTTGGGGGCCACCTTTACACCTGTTGCAGTCTCTGGGCATCTCCCATTTG 1531
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1569 AGCCACGTAATCTCTTGGAGACCTGCAATTGCGCAACACCTTTTAAAGGGAGGAGAGAG 1628
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1592 CACTTAGTTTCTGAAGTCTCTGGGACATCTCTGGGACCTTGAGCCTAGAGATTWRGTT 1648
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1629 CACTTAGTTT-TGAAGTCTCTGGGACATCTCTGGGACCTTGAGCCTAGAGATTTAGGT 1684
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RESULT 8
OCUS AR181083 1601 bp DNA linear PAT 20-APR-2002
SEQUENCE 24 from patent US 6335013.
AR181083
AR181083.1 GI:20223297

Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1601)
AUTHORS Ford,J., Mulero,J.J. and Yeung,G.
TITLE Methods and materials relating to CD39-like polypeptides
JOURNAL Patent: US 6335013-A 24 01-JAN-2002;
FEATURES Location/Qualifiers
source 1..1601
BASE COUNT 436 a 352 c 428 g 385 t
ORIGIN

Query Match 80.3%; Score 1445; DB 6; Length 1601;
Best local Similarity 100.0%; Pred. No. 0;
Matches 1445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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421 GAACTCGAATTCATGTTTACACCTTTTGTGAGAAAATGCCAGGACAGCTTCCAATCTAG 480
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QY 541 AGGGTGCTGAGACCGTTCAAGGGCTCTTAGAGGTGSCCAAAGACTCAATCCCCGAAGTC 600
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Db 541 AGGGTGCTGAGACCGTTCAAGGGCTCTTAGAGGTGSCCAAAGACTCAATCCCCGAAGTC 600
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Db 601 ACTGGAAGAACCCCAAGTCTCTAAAGGCAACAGCAGGACTACGCTTACTGCCAGAAC 660
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Db 721 TACCAAAGGGCAGTGTAGCATCATGGATGGATCCGACGAAGGCATATTAGCTTGGGTTA 780
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Db 841 ACCTAGGGGAGCCTCCACCCAAATCACGTTCCCTGCCCCAGTTTGAGAAAACCTCTGGAAC 900
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Db 901 AAACCTCTAGGGGCTACCTCACTTCTCTTTGAGATGTTTAAACAGCAGCTTATATAGCTCTATA 960
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Db 961 CACATAGTTACCTGGGATTTGGATTGAAAGCTGCAAGACTAGCAACCCCTGGAGCCCTGG 1020
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QY 1441 TACAG 1445
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Db 1441 TACAG 1445
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RESULT 9
AR227886
LOCUS AR227886 1601 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 24 from patent US 6447771.
ACCESSION AR227886
VERSION AR227886.1, GI:27266494
KEYWORDS

61 TGTGGAGTGTCTTGGCTGAATCCTCATACAGACAGATCATTTATGGTGTCTAGGTTGA 120
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1441 TACAG 1445
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RESULT 11
AR181065
LOCUS AR181065 1287 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 4 from patent US 6335013.
ACCESSION AR181065
VERSION AR181065.1 GI:20223279
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1287)
AUTHORS Ford,J., Mulero,J.J. and Yeung,G.
TITLE Methods and materials relating to CD39-like polypeptides
JOURNAL Patent: US 6335013-A 4 01-JAN-2002;
FEATURES Location/Qualifiers
source 1..1287
BASE COUNT 330 a 290 c 344 g 323 t
ORIGIN

Query Match 71.5%; Score 1287; DB 6; Length 1287;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1287; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 246 ATGGCCACTTCTTGGGGCACAGTCTTTTTCATGCTGGTGGTATCCTGTGTTGCGAGCGCT 305
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Db 1 ATGGCCACTTCTTGGGGCACAGTCTTTTTCATGCTGGTGGTATCCTGTGTTGCGAGCGCT 60
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QY 306 GTCTCCACAGGAACCCAGCAGACTTGGTTTGAGGGATCTTCTCTTCCATGTGCCCC 365
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Db 61 GTCTCCACAGGAACCCAGCAGACTTGGTTTGAGGGATCTTCTCTTCCATGTGCCCC 120
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Db 181 CGAATTCATGTTTACACCTTTGTGCAGAAAATGCCAGGACAGCTTCCAATTTCTAGAAGGG 240
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QY 486 GAAGTTTTTGTATTCTGTGAAGCCAGGACTTTCTGCTTTTGTAGATCAACCTTAAGCAGGGT 545
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b 421 GCCAAGGCTCTGCTCTTTGAGGTAAAGGAGATCTTCAGGAAGTCACTTTCTGGTACCA 480
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b 481 AAGGGCAGTGTAGCATCATGGATGGATCCGACGAAGGCATATTAGTTGGGTACTGTG 540
y 786 AATTTTCTGACAGGTGACATGGCCACAGACAGGAGACTGTGGGACCTTGGACCTA 845
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b 1261 TTGCAGTCTCTGGGCATCTCCCATTTGA 1287

RESULT 12
210058
JUS AR210058 1287 bp DNA linear PAT 20-JUN-2002
FINITION Sequence 4 from patent US 6387645.
SESSION AR210058
RSION AR210058.1 GI:21512190
WORDS
URCE Unknown.
ORGANISM Unknown.

Unclassified.
1 (bases 1 to 1287)
Ford, J. and Mulero, J.J.
Methods and materials relating to novel CD39-like polypeptides
Patent: US 6387645-A 4 14-MAY-2002;
Location/Qualifiers
source 1. 1287
/organism="unknown"
BASE COUNT 330 a 290 c 344 g 323 t
ORIGIN
Query Match 71.5%; Score 1287; DB 6; Length 1287;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1287; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 246 ATGGCCACTTCTTGGGGCACAGTCTTTTTCATGCTGGTGGTATCCTGTGTGTCAGCGCT 305
Db 1 ATGGCCACTTCTTGGGGCACAGTCTTTTTCATGCTGGTGGTATCCTGTGTGTCAGCGCT 60
QY 306 GTCTCCACAGGAACACAGACTTGGTTTGAGGGTATCTTCCCTGTCTTCCATGTGCCCC 365
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RESULT 13
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DEFINITION Sequence 4 from patent US 6447771.
ACCESSION AR227868
VERSION AR227868.1 GI:27266476
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1287)
AUTHORS Ford,J., Mulero,J.J. and Yeung,G.
TITLE Methods and materials relating to novel CD39-like polypeptides
JOURNAL Patent: US 6447771-A 4 10-SEP-2002;
FEATURES
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 size COUNT. 330 a 250 c 344 g 323 t
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Query Match 71.5%; Score 1287; DB 6; Length 1287;
Best Local Similarity 100.0%; Pred. No. 0;
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AR244597

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OCUS AR244597 1287 bp DNA linear PAT 20-DEC-2002
EFINITION Sequence 4 from patent US 6476211.
CESSION AR244597
ERSION AR244597.1 GI:27292462
EYWORDS
OURCE Unknown.
ORGANISM Unknown.
Unclassified.
1 (bases 1 to 1287)
AUTHORS Ford,J., Mulero,J.J. and Yeung,G.
TITLE Methods and materials relating to CD39-like polypeptides
JOURNAL Patent: US 6476211-A 4 05-NOV-2002;
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RESULT 15
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DEFINITION diphosphohydrolase 5, clone MSC:9:1:27 IMAGE:3847878, mRNA, complete
cds.
ACCESSION BC020966
VERSION BC020966.1 GI:18089246
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3157)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (03-JAN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
COMMENT Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www-shgc.stanford.edu>
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAX Plate: 20 Row: j Column: 19
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 4557426.

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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8	1277.4	71.0	1287	21	AAZ50357	Human CD39-L4 vari	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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21	342.2	19.0	2762	22	AAF63422	Human CD39-L2 spli
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25	339	18.8	2564	22	AAK94892	Human full-length
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28	320.8	17.8	475	23	ABV34226	Human prostate exp
29	320.6	17.8	2371	22	AAF63416	Human CD39-L2 spli
30	320.6	17.8	2497	22	AAF63421	Human CD39-L2 spli
31	320	17.8	342	24	ABV88403	Human colon cancer
32	303.6	16.9	9365	21	AAZ50359	Human CD39-L4 geno
33	303.6	16.9	9365	22	AAF63405	Human CD39 like pr
34	300.6	16.7	458	22	AAL24301	Human breast cance
35	300	16.7	300	21	AAZ50360	EST to isolate hum
36	300	16.7	300	22	AAF63388	Human cDNA used to
37	296.6	16.5	2294	22	AAF63419	Human CD39-L2 spli
38	294.6	16.4	855	22	AAL14095	Human breast cance
39	290.8	16.2	1498	22	AAF63387	cDNA encoding matu
40	290.8	16.2	2805	22	AAF63420	Human CD39-L2 spli
41	290.2	16.1	1002	22	AAK82209	Human immune/haema
42	290.2	16.1	14747	22	AAF63406	Human CD39 like pr
43	290.2	16.1	15977	22	AAF63407	Human CD39 like pr
44	284.6	15.8	442	22	AAL15455	Human breast cance
45	282.4	15.7	404	23	ABV03936	Human prostate exp

ALIGNMENTS

RESULT :			
AAZ50356 .			
ID	AAZ50356 standard; cDNA; 1799 BP.		
XX			
AC	AAZ50356;		
DT	18-MAY-2000 (first entry)		
XX			
DE	Human CD39-L4 protein encoding cDNA.		
XX			
KW	CD39-L4; human; apyrase; nucleotide diphosphatase; NCPase;		
KW	ATP Diphosphohydrolase; Atpbase; adenosine diphosphate; ADP; treatment;		
KW	platelet aggregation; antithrombotic; thrombosis; myocardial infarction;		
KW	cerebral ischaemia; angina; vascular graft; extracorporeal circulation;		
KW	molecular weight marker; nutritional supplement; tumour; prevention;		
XX	drug targeting; ss.		
CS	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
FT	CDS	246..1532	
FT		/*tag= a	
FT		/product= "Human CD39-L4 protein"	
FT		/note= "Homologous to the CD39 family"	
FT	sig_peptide	246..311	
FT		/*tag= b	
FT		/note= "Comprises hydrophobic stretch of amino acids"	
FT	mat_peptide	312..1529	
FT		/*tag= c	
FT		/product= "Mature human CD39-L4 protein"	
FT		/note= "Homologous to human and murine CD39"	

X WO200004041-A2.
X
X
D 27-JAN-2000.
X
F 16-JUL-1999; 99WO-US16180.
X
R 16-JUL-1998; 98US-0118205.
R 24-JUL-1998; 98US-0122449.
R 04-FEB-1999; 99US-0244444.
R 19-MAR-1999; 99US-0273447.
R 09-JUL-1999; 99US-0350836.
X
X (HYSE-) HYSEQ INC.
A
X Ford J, Mulero J;
X
R WPI; 2000-182397/16.
R P-PSDB; AAY44849.
X
T New nucleic acid encoding human CD39-like protein, useful for treating
T and preventing thrombotic disease -
X
S Claim 8; Fig 1; 125pp; English.
X
C The present sequence is a cDNA encoding the CD39-L4 protein, an apyrase
C and/or nucleotide diphosphatase (NDPase). It is isolated from the human
C foetal liver-spleen cDNA library, b2HFLS20W. It is a soluble ATP
C Diphosphohydrolases (ATPDase) and is involved in the hydrolysis of
C adenosine diphosphate (ADP), the agonist that causes platelet
C aggregation. CD39-L4 protein has 30% and 80% homology to human and
C murine CD39. It has platelet aggregation inhibition and antithrombotic
C activity. CD39-L4 is used to treat or prevent thrombosis, myocardial
C infarction, cerebral ischaemia and angina. It is also used in vitro, to
C maintain vascular grafts or during extracorporeal circulation, to
C hydrolyse NDP, as molecular weight markers and as nutritional
C supplements. It is used to identify therapeutic agents that bind and
C modulate CD39-L4. It is coupled to toxins for targeting drugs to tumours
C or other cells that express CD39-L4.
X
Q Sequence 1799 BP; 467 A; 409 C; 472 G; 442 T; 9 other;

Query Match 99.8%; Score 1794.8; DB 21; Length 1799;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1799; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 GCGGGCTGCCGCGCAAGGGTGGCGCGCGCGGTTTCCCTTGTCTCGTCACAGAGAA 60
b 1 GCGGGCTGCCGCGCAAGGGTGGCGCGCGCGGTTTCCCTTGTCTCGTCACAGAGAA 60

Y 61 TGTGGAGTGCTTGGCTGAATCCTCATACAGACAGATCATATATGGTGTCTGTAGTTGA 120
b 61 TGTGGAGTGCTTGGCTGAATCCTCATACAGACAGATCATATATGGTGTCTGTAGTTGA 120

Y 121 AAAAGTGATATAATAAAGGAACCAAGAGAGAAATTCAGAGAGAGAGAGAGAGAGAG 180
b 121 AAAAGTGATATAATAAAGGAACCAAGAGAGAAATTCAGAGAGAGAGAGAGAGAGAG 180

Y 181 GCAGGTGTGGAGCAGGAGATTGCTTCTGCAACAAAGCCCTCACCCAGCCACATCTTGGGA 240
b 181 GCAGGTGTGGAGCAGGAGATTGCTTCTGCAACAAAGCCCTCACCCAGCCACATCTTGGGA 240

Y 241 AAAGAAATGGCCACTTCTTGGGCGACAGTCTTTTTCATGCTGGTGGTATCCTGTGTTGCA 300
b 241 AAAGAAATGGCCACTTCTTGGGCGACAGTCTTTTTCATGCTGGTGGTATCCTGTGTTGCA 300

Y 301 GCGCTGTCTCCACAGGAACCCAGCAGACTTGGTTTGGAGGTATCTTCCCTGTCTCCATGT 360
b 301 GCGCTGTCTCCACAGGAACCCAGCAGACTTGGTTTGGAGGTATCTTCCCTGTCTCCATGT 360

Y 361 GCCCCATCAATGTCAGCGCCAGCACCTTGTATGGAATTATGTTTATGTCAGGGAGCACTG 420
b 361 GCCCCATCAATGTCAGCGCCAGCACCTTGTATGGAATTATGTTTATGTCAGGGAGCACTG 420

QY 421 GAACTCGAATTCATGTTTACACCTTTTGTGAGAAAAATGCCAGGACAGCTTCCAATTTCTAG 480
Db 421 GAACTCGAATTCATGTTTACACCTTTTGTGAGAAAAATGCCAGGACAGCTTCCAATTTCTAG 480

QY 481 AAGGGGAAGTTTTTGATTTCTGTGAAGCCAGACTTTTCTGCTTTTGTAGATCAACCTAAGC 540
Db 481 AAGGGGAAGTTTTTGATTTCTGTGAAGCCAGACTTTTCTGCTTTTGTAGATCAACCTAAGC 540

QY 541 AGGGTGTGAGACCGTTCAAGGGCTCTTAGAGGTGGCCAAAGACTCAATCCCCGAAGTC 600
Db 541 AGGGTGTGAGACCGTTCAAGGGCTCTTAGAGGTGGCCAAAGACTCAATCCCCGAAGTC 600

QY 601 ACTGGAAAAAGACCCCGAGTGGTCTTAAAGGCAACAGCAGGACTACGCTTACTGCCAGAAC 660
Db 601 ACTGGAAAAAGACCCCGAGTGGTCTTAAAGGCAACAGCAGGACTACGCTTACTGCCAGAAC 660

QY 661 ACAAAGCCAAGGCTCTGCTCTTTGAGGTAAAGGAGATCTTCAGGAAAGTCACTTTCCCTGG 720
Db 661 ACAAAGCCAAGGCTCTGCTCTTTGAGGTAAAGGAGATCTTCAGGAAAGTCACTTTCCCTGG 720

QY 721 TACCAAGGGCGAGTGTAGCATCATGGATCCGACGAAGGCATATTAGCTTGGGTTA 780
Db 721 TACCAAGGGCGAGTGTAGCATCATGGATCCGACGAAGGCATATTAGCTTGGGTTA 780

QY 781 CTGTGAATTTTCTGACAGGTCAGCTGCATGCCACACAGCAGGAGACTGTGGGACCTTGG 840
Db 781 CTGTGAATTTTCTGACAGGTCAGCTGCATGCCACACAGCAGGAGACTGTGGGACCTTGG 840

QY 841 ACCTAGGGGGAGCCCTCCACCCAAATCACGTTCTGCCCCAGTTTGAAGAAACTCTGGAAC 900
Db 841 ACCTAGGGGGAGCCCTCCACCCAAATCACGTTCTGCCCCAGTTTGAAGAAACTCTGGAAC 900

QY 901 AAACTCCTAGGGGCTACCTCACCTTCTTTGAGATGTTTAAACAGCAGCTTATAAGCTCTATA 960
Db 901 AAACTCCTAGGGGCTACCTCACCTTCTTTGAGATGTTTAAACAGCAGCTTATAAGCTCTATA 960

QY 961 CACATAGTTACCTGGGATTTGGATTGAAAGCTGCAAGACTAGCAACCTGGGAGCCCTGG 1020
Db 961 CACATAGTTACCTGGGATTTGGATTGAAAGCTGCAAGACTAGCAACCTGGGAGCCCTGG 1020

QY 1021 AGACAGAAGGGACTGATGGGCACACTTTCCGAGTGCCTGTTTACCGAGATGTTGGAAG 1080
Db 1021 AGACAGAAGGGACTGATGGGCACACTTTCCGAGTGCCTGTTTACCGAGATGTTGGAAG 1080

QY 1081 CAGAGTGGATCTTTGGGGTGTGAATATACAGTATGGTGGCAACCAAGAAAGGGAGGTGG 1140
Db 1081 CAGAGTGGATCTTTGGGGTGTGAATATACAGTATGGTGGCAACCAAGAAAGGGAGGTGG 1140

QY 1141 GCTTTGAGCCCTGCTATGCCGAAGTGTGAGGGTGGTACGAGGAAACTTCAACAGCCAG 1200
Db 1141 GCTTTGAGCCCTGCTATGCCGAAGTGTGAGGGTGGTACGAGGAAACTTCAACAGCCAG 1200

QY 1201 AGGAGGTCCAGAGAGGTTCTTCTATGCTTTCTTACTATTATGACCGAGCTGTTGACA 1260
Db 1201 AGGAGGTCCAGAGAGGTTCTTCTATGCTTTCTTACTATTATGACCGAGCTGTTGACA 1260

QY 1261 CAGACATGATTGATTGAAAAAGGGGGTATTTTAAAGTTGAAGATTTGAAAGAAAAG 1320
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QY 1321 CCAGGGAAGTGTGTGATAACTTTGGAAAACTTCACTCAGGCAGTCCCTTCTGTGCATGG 1380
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QY 1381 ATCTCAGCTACATCAGACCCCTGTTAAAGGATGGCTTTGGCTTTGCAGACAGCAGTCT 1440
Db 1381 ATCTCAGCTACATCAGACCCCTGTTAAAGGATGGCTTTGGCTTTGCAGACAGCAGTCT 1440

QY 1441 TACAGCTCAGAAAGAGTGAACAACATAGAGACGGGCTGGGCTTGGGGGCCACCTTTC 1500
Db 1441 TACAGCTCAGAAAGAGTGAACAACATAGAGACGGGCTGGGCTTGGGGGCCACCTTTC 1500

781 CTGTGAATTTTCTGACAGGTCAGCTGCATGGCCACAGACAGGAGACTGTGGGACCTTGG 840
|||||
781 CTGTGAATTTTCTGACAGGTCAGCTGCATGGCCACAGACAGGAGACTGTGGGACCTTGG 840
841 ACCTAGGGGAGCCTCCACCCAAATCACGTTTCTGCCCCAGTTTGAGAAAACTCTGGAAC 900
|||||
841 ACCTAGGGGAGCCTCCACCCAAATCACGTTTCTGCCCCAGTTTGAGAAAACTCTGGAAC 900
901 AAACCTCCTAGGSGCTACCTCACCTTCTTTGAGATGTTTACAGACACTTATAAGCTCTATA 960
|||||
901 AAACCTCCTAGGSGCTACCTCACCTTCTTTGAGATGTTTACAGACACTTATAAGCTCTATA 960
961 CACATAGTTACCTGGGATTTGGATTGAAAGCTGCAAGACTAGCAACCTTGGGAGCCTTG 1020
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1021 AGACAGAAAGGACTGATGGGCACACCTTCCGGAGTGCCCTGTTTACCGAGATGTTGGAAG 1080
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1021 AGACAGAAAGGACTGATGGGCACACCTTCCGGAGTGCCCTGTTTACCGAGATGTTGGAAG 1080
1081 CAGAGTGGATCTTTGGGGGTGTGAATATACCAGTATGTTGGCAACCAAGAGGGGAGGTGG 1140
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1081 CAGAGTGGATCTTTGGGGGTGTGAATATACCAGTATGTTGGCAACCAAGAGGGGAGGTGG 1140
1141 GCTTTGAGCCCTGCTATGCCGAAGTGTGAGGGTGGTACGAGAAACTTCCACCAACCCAG 1200
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1201 AGGAGGTCAGAGAGGTTCCCTCTATGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1260
|||||
1201 AGGAGGTCAGAGAGGTTCCCTCTATGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1260
1261 CAGACATGATTGATTTATGAAAGGGGGTATTTTAAAGTTGAAGATTTTGAAGAAAG 1320
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1321 CCAGGGAAGTGTGTGATAAATTTGGAACCTTCACTCAGGCACTTCTTCTTCTTCTTCTTCT 1380
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1321 CCAGGGAAGTGTGTGATAAATTTGGAACCTTCACTCAGGCACTTCTTCTTCTTCTTCTTCT 1380
1381 ATCTCAGCTACATCACAGCCCTGTTTAAAGGATGGCTTTGGCTTGGCTTGGCTTGGCTTGG 1440
|||||
1381 ATCTCAGCTACATCACAGCCCTGTTTAAAGGATGGCTTTGGCTTGGCTTGGCTTGGCTTGG 1440
1441 TACAGCTCACAAAGAAAGTGAACAACATAGAGACGGGCTGGGCTTGGGGCCACCTTTC 1500
|||||
1441 TACAGCTCACAAAGAAAGTGAACAACATAGAGACGGGCTGGGCTTGGGGCCACCTTTC 1500
1501 ACCTGTTGCAGTCTCTGGGCATCTCCCAATGAGGCCACGTAATCTTGGAGACCTTGCAT 1560
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1501 ACCTGTTGCAGTCTCTGGGCATCTCCCAATGAGGCCACGTAATCTTGGAGACCTTGCAT 1560
1561 TTGCCAACACCTTTTAAGGGGAGGAGAGACACTTAGTTTCTGAACTAGTCTGGGGACA 1620
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1561 TTGCCAACACCTTTTAAGGGGAGGAGAGACACTTAGTTTCTGAACTAGTCTGGGGACA 1620
1621 TCCTGGACTTGACCTAGAGATTWRGTTAATTAASCGGCCGAGCTTATCCTTWTATRAGGT 1680
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1621 TCCTGGACTTGACCTAGAGATTWRGTTAATTAASCGGCCGAGCTTATCCTTWTATRAGGT 1680
1681 AATTTACTTGCMTGGCCCGCTTTTACACGTCGTGATGNNAACTCGCTCCCAACTAACGC 1740
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1681 AATTTACTTGCMTGGCCCGCTTTTACACGTCGTGATGNNAACTCGCTCCCAACTAACGC 1740
1741 TTGASAMATCCCCTTTCGCAGCTGCGATACCAAAAGCCGACGACGCTTCCACAGTGGCA 1799
|||||
1741 TTGASAMATCCCCTTTCGCAGCTGCGATACCAAAAGCCGACGACGCTTCCACAGTGGCA 1799

ESULT 3
AA96068
D AAA96068 standard; DNA; 1998 BP.
X

AAA96068;
29-JAN-2001 (first entry)
Human ecto-phosphatase CD39L4 coding sequence.
Drug resistance; ATP gradient; chemotherapeutic; antibiotic; herbicide;
human; ecto-phosphatase; extra-cellular phosphatase; ds.
Homo sapiens.
WO200052144-A1.
08-SEP-2000.
28-FEB-2000; 2000WO-US05315.
03-MAR-1999; 99US-0261825.
(TEXA) UNIV TEXAS.
Thomas CE, Windsor JB, Roux SJ, Lloyd AM, Hurley L;
MPI; 2000-587306/55.
Increasing or decreasing drug resistance in target bacteria, yeast,
plant or mammalian cells comprises altering ATP gradient across
biological membrane of target cell -
Claim 14; Page -; 85pp; English.
The present invention relates to a method for increasing or decreasing
drug resistance in target bacteria, yeast, plant or mammalian cells by
altering the ATP gradient across the biological membrane of the target
cell. The method is useful for modulating drug resistance of cells. It
is useful for increasing the sensitivity of cells to chemotherapeutic
and antibiotic agents and increasing resistance to herbicides. The
present sequence is human CD39L4 coding sequence. This sequence encodes
an extra-cellular phosphatase (ecto-phosphatase) and was used in the
present invention to modulate drug resistance.
Note: The present sequence is not shown in the specification, but is
referred to via its GenBank accession number.
Sequence 1998 BP; 557 A; 449 C; 491 G; 501 T; 0 other;
Query Match 87.5%; Score 1575; DB 21; Length 1998;
Best Local Similarity 98.2%; Pred. No. 0;
Matches 1620; Conservative 2; Mismatches 2; Indels 25; Gaps 2;
QY 24 GCGGCGCGTTCCTTGTTCCTGGTCAACAAAGAAATGTGGAGTGTCTTGGCTGAATCC 83
|||||
Db 1 GCGGCGCGTTCCTTGTTCCTGGTCAACAAAGAAATGTGGAGTGTCTTGGCTGAATCC 60
QY 84 TCATACAGACAAGATCATTATGGTGTGTT-----AGGTTG 119
|||||
Db 61 TCATACAGACAAGATCATTATGGTGTGTTAGGTAGACTTGTATCCAGATGTAAAGTTG 120
QY 120 AAAAAGTGATATAATAAAGGAACCAAGGAGAAAATTCAGAAAGGAAAGAAAATTCCTC 179
|||||
Db 121 AAAAAGTGATATAATAAAGGAACCAAGGAGAAAATTCAGAAAGGAAAGAAAATTCCTC 180
QY 180 TGCAGGTGTGCGAGCAGGATTCCTTCTGCAACAAAGCCCTCCACCCAGCCACATCTTGGG 239
|||||
Db 181 TGCAGGTGTGCGAGCAGGATTCCTTCTGCAACAAAGCCCTCCACCCAGCCACATCTTGGG 240
QY 240 AAAAGAAATGGCCACTTCTTGGGGCACAGTCTTTTTCATGCTGGTGGTATCCTGTGTTTC 299
|||||
Db 241 AAAAGAAATGGCCACTTCTTGGGGCACAGTCTTTTTCATGCTGGTGGTATCCTGTGTTTC 300
QY 300 AGCGCTGTCTCCACAGGAACCCAGCAGACTTGGTTTACGGGTATCTTCTGTCTTCCCATG 359
|||||
Db 301 AGCGCTGTCTCCACAGGAACCCAGCAGACTTGGTTTACGGGTATCTTCCGTCTTCCCATG 360

360 TGCCCCATCAATGTCAGGCCAGCACCTTGATGGAATTATGTTTGTATGACGGGAGCACT 419
|||||
361 TGCCCCATCAATGTGACGCGCAGCACCTTGATGGAATTATGTTTGTATGACGGGAGCACT 420
|||||
420 GGAACCTCGAATTCATGTTTACACCTTTGTGCAGAAATGCCAGGACAGCTTCCAATTCTA 479
|||||
421 GGAACCTCGAATTCATGTTTACACCTTTGTGCAGAAATGCCAGGACAGCTTCCAATTCTA 480
|||||
480 GAAGGGGAAGTTTGTGATTCGTGTGAAGCCAGGACTTCTGCTTTTGTAGATCAACCTAAG 539
|||||
481 GAAGGGGAAGTTTGTGATTCGTGTGAAGCCAGGACTTCTGCTTTTGTAGATCAACCTAAG 540
|||||
540 CAGGGTGCTGAGACCGTTCAAGGGCTCTTAGAGGTGGCCAAAGACTCAATCCCCCGAAGT 599
|||||
541 CAGGGTGCTGAGACCGTTCAAGGGCTCTTAGAGGTGGCCAAAGACTCAATCCCCCGAAGT 600
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600 CACTGGAAAAAGACCCCGAGTGGTCTCTAAAGGCAACAGCAGGACTACGCTTACTGCCAGAA 659
|||||
601 CACTGGAAAAAGACCCCGAGTGGTCTCTAAAGGCAACAGCAGGACTACGCTTACTGCCAGAA 660
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660 CACAAAGCCAAAGGCTCTGCTCTTTGAGGTAAAGGAGATCTTCAGGAAGTCACCTTTCCCTG 719
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661 CACAAAGCCAAAGGCTCTGCTCTTTGAGGTAAAGGAGATCTTCAGGAAGTCACCTTTCCCTG 720
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720 GTACCAAAGGGCAGTGTTAGCATCATGGATCGACGAAGGCATATTAGCTTGGGTT 779
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721 GTACCAAAGGGCAGTGTTAGCATCATGGATCGACGAAGGCATATTAGCTTGGGTT 780
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780 ACTGTGAATTTTCTGACAGGTTCAGCTGCATGGCCACAGACAGGAGACTGTGGGGACCTTG 839
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781 ACTGTGAATTTTCTGACAGGTTCAGCTGCATGGCCACAGACAGGAGACTGTGGGGACCTTG 840
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840 GACCTAGGGGGAGCCTCCACCAAAATCACGTTTCCTGCCCCAGTTTGAGAAAACCTCTGGAA 899
|||||
841 GACCTAGGGGGAGCCTCCACCAAAATCACGTTTCCTGCCCCAGTTTGAGAAAACCTCTGGAA 900
|||||
900 CAAACTCCTAGGGGCTACCTCACTTCCTTTTGAGATGTTTAAACAGCACCTTATAAGCTCTAT 959
|||||
901 CAAACTCCTAGGGGCTACCTCACTTCCTTTTGAGATGTTTAAACAGCACCTTATAAGCTCTAT 960
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960 ACACATAGTTTACCTGGGATTTGGATTGAAAGCTGCAAGACTAGCAACCCCTGGAGCCCTG 1019
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961 ACACATAGTTTACTTGGGATTTGGATTGAAAGCTGCAAGACTAGCAACCCCTGGAGCCCTG 1020
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1020 GAGACAGAAGGGACTGATGGGCACACTTTCCTGGAGTGCTGTTTACCGAGATGGTTGGAA 1079
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1021 GAGACAGAAGGGACTGATGGGCACACTTTCCTGGAGTGCTGTTTACCGAGATGGTTGGAA 1080
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1141 GGCCTTTGAGCCCTGCTATGCCGAAGTGCTGAGGGTGTTACGAGGAAAACCTTCACCAAGCCA 1200
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1200 GAGGAGGTCCAGAGAGGTTCCTTCTATGCTTTCCTTACTATTATGACCGAGCTGTTGAC 1259
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1201 GAGGAGGTCCAGAGAGGTTCCTTCTATGCTTTCCTTACTATTATGACCGAGCTGTTGAC 1260
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1260 ACAGACATGATTGATTATGAAAAGGGGGTATTTTAAAGTTGAAGATTTTGAAGAAA 1319
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1261 ACAGACATGATTGATTATGAAAAGGGGGTATTTTAAAGTTGAAGATTTTGAAGAAA 1320
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1320 GCCAGGGAAGTGTGTGATAACTTGGAAAACTTCACCTCAGCAGTCCCTTTCCTGTGCATG 1379
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1321 GCCAGGGAAGTGTGTGATAACTTGGAAAACTTCACCTCAGCAGTCCCTTTCCTGTGCATG 1380
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1380 GATCTCAGCTACATCACAGCCCTGTTAAAGGATGGCTTTGGCTTTGCAGACAGCACAGTC 1439
|||||
1381 GATCTCAGCTACATCACAGCCCTGTTAAAGGATGGCTTTGGCTTTGCAGACAGCACAGTC 1440
|||||
1440 TTACAGCTCACAAAAGAAAGTGAACAAACATAGAGACGGGCTTGGGCTTGGGGGCCACCTTT 1499
|||||

Db 1441 TTACAGCTCACAAAGAAAGTGAACAAACATAGAGACGGGCTGGCCCTTGGGGCCACCTTT 1500
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Qy 1500 CACCTGTTGCAGTCTCTGGGCATCTCCCATTTGAGGCCACGCTACTTCCCTTGGAGACCTGCA 1559
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Db 1501 CACCTGTTGCAGTCTCTGGGCATCTCCCATTTGAGGCCACGCTACTTCCCTTGGAGACCTGCA 1560
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Qy 1560 TTTGCCAACACCTTTTAAAGGGGAGGAGAGACACTTAGTTTCTGAACTAGTCTGGGGAC 1619
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Db 1561 TTTGCCAACACCTTTTAAAGGGGAGGAGAGACACTTAGTTTCTGAACTAGTCT-GGGAC 1619
|||||
Qy 1620 ATCTGGACTTGAGCCTAGAGATTNRGTT 1648
|||||
Db 1620 ATCTGGACTTGAGCCTAGAGATTTAGGT 1648
|||||
RESULT 4
AAD31695
ID AAD31695 standard; cDNA; 1998 BP.
XX
AC AAD31695;
XX
DT 18-JUN-2002 (first entry)
XX
DE Human CD39L4 cDNA;
XX
KW Human; CD-39-like protein; CD39L4 protein; therapy; immune deficiency;
KW autoimmune disorder; multiple sclerosis; systemic lupus erythematosus;
KW rheumatoid arthritis; autoimmune thyroiditis; allergic reaction; asthma;
KW insulin dependent diabetes mellitus; periodontal disease; osteoporosis;
KW osteoarthritis; wound healing; tissue repair; Alzheimer's disease; ulcer;
KW Parkinson's disease; amyotrophic lateral sclerosis; Huntington's disease;
KW nervous system disease; nerve injury; ischaemia-reperfusion injury;
KW endotoxin lethality; arthritis; nephritis; inflammatory bowel disease;
KW Crohn's disease; virucide; antibacterial; antifungal; neuroprotective;
KW dermatological; immunosuppressive; vulnery; nootropic; anticonvulsant;
KW antiinflammatory; nephrotropic; gastrointestinal; vasotropic;
KW chromosome 14q24; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
CDS 247..1533
FT /*tag= a
FT /product= "Human CD39L4 protein."
XX
ZN US6350447-B1.
XX
PD 26-FEB-2002.
XX
PF 29-JAN-1999; 99US-0240639.
XX
PR 29-JAN-1999; 99US-0240639.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Chadwick BP, Frischauf A;
XX
XX
DR WP1; 2002-215262/27.
DR P-PSDB; AAE19883.
XX
XX An isolated polypeptide with phosphohydrolase activity, designated
PT CD39L2, useful to identify other proteins with which binding occurs or
PT identify inhibitors and for treatment of, e.g., Alzheimer's, multiple
PT sclerosis and osteoporosis -
XX
PS Example; Fig 7; 101pp; English.
XX
CC The present invention relates to novel proteins with phosphohydrolase
CC activity, designated CD-39-like (CD39L) proteins and polynucleotides
CC encoding such proteins. CD39L proteins are useful to treat infectious
CC diseases caused by viral, bacterial, fungal or other infection that may
CC be treatable with CD39L. They are useful in the treatment of various

C immune deficiencies and disorders, autoimmune disorders such as multiple
C sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune
C thyroiditis and insulin dependent diabetes mellitus, allergic reactions
C and conditions such as asthma and other respiratory problems, periodontal
C disease, osteoporosis, osteoarthritis and other tooth repair processes.
C They may have utility in compositions used for bone, cartilage, tendon,
C ligament and/or nerve tissue growth or regeneration as well as for wound
C healing and tissue repair and replacement and in the treatment of burns,
C incisions and ulcers. CD39L proteins may also be useful for proliferation
C of neural cells and for regeneration of nerve and brain tissue, i.e. for
C the treatment of central nervous system diseases such as Alzheimer's
C disease, Parkinson's disease, amyotrophic lateral sclerosis, Huntington's
C disease, peripheral nervous system diseases peripheral nerve injuries,
C peripheral neuropathy and localised neuropathies. They are also used to
C treat mechanical and traumatic disorders which involve degeneration,
C death or trauma to neural cells or nerve tissue. CD39L proteins of the
C invention are also useful to promote better or faster closure of non-
C healing wounds, including pressure ulcers, ulcers associated with
C vascular insufficiency and surgical and traumatic wounds. They also
C exhibit anti-inflammatory activity and may be used to treat inflammatory
C conditions including chronic or acute conditions), including ischaemia-
C reperfusion injury, endotoxin lethality, arthritis, nephritis, cytokine
C or chemokine-induced lung injury, inflammatory bowel disease or Crohn's
C disease. The present sequence is human CD39L4 DNA. CD39L4 gene is
C localised on chromosome 14q24.

X Sequence 1998 BP; 557 A; 449 C; 491 G; 501 T; 0 other;

Query Match	87.5%;	Score 1575;	DB 24;	Length 1998;
Best Local Similarity	98.2%;	Pred. No. 3;		
Matches 1620;	Conservative	2;	Mismatches	2;
			Indels	25;
			Gaps	2;
Y 24	GC	GC	GC	GC
b 1	GC	GC	GC	GC
Y 84	TC	TC	TC	TC
b 61	TC	TC	TC	TC
Y 120	AA	AA	AA	AA
b 121	AA	AA	AA	AA
Y 180	TG	TG	TG	TG
b 181	TG	TG	TG	TG
Y 240	AA	AA	AA	AA
b 241	AA	AA	AA	AA
Y 300	AG	AG	AG	AG
b 301	AG	AG	AG	AG
Y 360	TG	TG	TG	TG
b 361	TG	TG	TG	TG
Y 420	GG	GG	GG	GG
b 421	GG	GG	GG	GG
Y 480	GA	GA	GA	GA
b 481	GA	GA	GA	GA
Y 540	CA	CA	CA	CA
b 541	CA	CA	CA	CA
Y 600	CA	CA	CA	CA

RESULT 5

Db 601	CA	CA	CA	CA
Qy 660	CA	CA	CA	CA
Db 661	CA	CA	CA	CA
Qy 720	GT	GT	GT	GT
Db 721	GT	GT	GT	GT
Qy 780	AC	AC	AC	AC
Db 781	AC	AC	AC	AC
Qy 840	GA	GA	GA	GA
Db 841	GA	GA	GA	GA
Qy 900	CA	CA	CA	CA
Db 901	CA	CA	CA	CA
Qy 960	AC	AC	AC	AC
Db 961	AC	AC	AC	AC
Qy 1020	GA	GA	GA	GA
Db 1021	GA	GA	GA	GA
Qy 1080	GC	GC	GC	GC
Db 1081	GC	GC	GC	GC
Qy 1140	GG	GG	GG	GG
Db 1141	GG	GG	GG	GG
Qy 1200	GAG	GAG	GAG	GAG
Db 1201	GAG	GAG	GAG	GAG
Qy 1260	AC	AC	AC	AC
Db 1261	AC	AC	AC	AC
Qy 1320	GC	GC	GC	GC
Db 1321	GC	GC	GC	GC
Qy 1380	GA	GA	GA	GA
Db 1381	GA	GA	GA	GA
Qy 1440	TT	TT	TT	TT
Db 1441	TT	TT	TT	TT
Qy 1500	CA	CA	CA	CA
Db 1501	CA	CA	CA	CA
Qy 1560	TT	TT	TT	TT
Db 1561	TT	TT	TT	TT
Qy 1620	AT	AT	AT	AT
Db 1620	AT	AT	AT	AT

QY	61	TGTGGAGTGTCTTGGCTGAATCCTCATACAGACAAGATCATTTATGGTGCCTGTTAGGTTGA	120
DB	61		120
QY	121	AAAAGTGATATAATAAAGGAACCAAGGAGAAAAATTCAGAAAGGAAAGAAAAAATTCGCCTCT	180
DB	121		180
QY	181	GCAGGTGTGGAGCAGGATTGCTTCTGCAACAAAGCCCTCCACCCAGCCACATCTTGGGA	240
DB	181		240
QY	241	AAAGAAATGGCCACTTCTTGGGGCACAGTCTTTTTCATGCTGGTGGTATCCTGTGTTTGCA	300
DB	241		300
QY	301	GCAGGTGTGGAGCAGGATTGCTTCTGCAACAAAGCCCTCCACCCAGCCACATCTTGGGA	360
DB	301		360
QY	361	GCCCCATCAATGTCAGGCCAGCACCTTGTATGGAATATGTTGATGCAGGGAGCACTG	420
DB	361		420
QY	421	GAACTCGAATTCATGTTTACACCTTTGTGCAGAAAAATGCCAGCAGACTTCCAATCTAG	480
DB	421		480
QY	481	AAGGGGAAGTTTTTGTGATCTGTGAAGCCAGGACTTTCTGCTTTTGTAGATCAACCTAAGC	540
DB	481		540
QY	541	AGGGTGTGAGACCGTTCAGGGCTCTTAGAGGTGGCCAAAGACTCAATCCCCGGAAGTC	600
DB	541		600
QY	601	ACTGAAAAAGACCCAGTGGTCTTAAGGGAACAGCAGGACTACGTTACTGCCAGAAC	660
DB	601		660
QY	661	ACAAAGCCAAAGGCTCTGCTCTTTGAGGTAAGGAGATCTTCAGGAGTCACTTTCTCTGG	720
DB	661		720
QY	721	TACCAAAGGGCAGTGTAGCATCATGATGGATCCGACGAAGGCATATTAGCTTGGGTTA	780
DB	721		780
QY	781	CTGTGAATTTTCTGACAGGTCAGCTGCATGGCCACAGACAGGAGACTGTGGGACCTTGG	840
DB	781		840
QY	841	ACCTAGGGGGAGCCCTCCACCCAAATCACGTTCTCTGCCCCAGTTTGAGAAAACTCTGGAAC	900
DB	841		900
QY	901	AAACTCTTAGGGGTACCTCACTTCTCTTTGAGATGTTTAAACAGCACTTATAAGCTCTATA	960
DB	901		960
QY	961	CACATAGTTACCTGGGATTGGATTGAAAGCTGCAAGACTAGCAACCTCGGAGCCCTGG	1020
DB	961		1020
QY	1021	AGACAGAAGGGACTGATGGGCACACTTTTCCGGAGTGCCTGTTTACCGAGATGGTTGGAAG	1080
DB	1021		1080
QY	1081	CAGAGTGGATCTTTGGGGTGTGAAATACCAAGTATGGTGGCAACCAAGAGGGGAGGTGG	1140
DB	1081		1140
QY	1141	GCTTTGAGCCCTGCTATGCCGAAGTGTGAGGGTGGTACGAGGAAGACTTCAACAGCCAG	1200

1141 GCATTGAGCCCTGCTATGCCGAAGTCTGAGGGTGGTACGAGGAAACCTCACCAGCCAG 1200
1201 AGGAGGTCACAGAGAGGTTCTCTATGCTTTCTCTACTATTATGACCGAGCTGTGACA 1260
1201 AGGAGGTCACAGAGAGGTTCTCTATGCTTTCTCTACTATTATGACCGAGCTGTGACA 1260
1261 CAGACATGATTGATTATGAAAAGGGGGTATTTTAAAAGTTGAAGATTTTGAAGAAAAG 1320
1261 CAGACATGATTGATTATGAAAAGGGGGTATTTTAAAAGTTGAAGATTTTGAAGAAAAG 1320
1321 CCAGGGAAGTGTGTGATACCTTGGAAAACTTCACCTCAGGCAGTCCTTTCTGTGCATGG 1380
1321 CCAGGGAAGTGTGTGATACCTTGGAAAACTTCACCTCAGGCAGTCCTTTCTGTGCATGG 1380
1381 ATCTCAGCTACATCAGAGCCCTGTTAAAGGATGGCTTTGGCTTTGCAGACAGCAGTCT 1440
1381 ATCTCAGCTACATCAGAGCCCTGTTAAAGGATGGCTTTGGCTTTGCAGACAGCAGTCT 1440
1441 TACAG 1445
1441 TACAG 1445

RESULT 6
AF63384
D AAF63384 standard; cDNA; 1601 BP.
X
C AAF63384;
X
T 14-MAY-2001 (first entry)
X
E Human cDNA encoding CD39 like protein CD39-L4.
X
W Human CD39-like protein; apyrase; NDPase; platelet function inhibitor;
W myocardial infarction; cerebral ischaemia; angina; arterial thrombosis;
W cerebral artery thrombosis; platelet aggregation; inflammation;
W apoptosis; autoimmune disorder; neurological disorder;
W Alzheimer's disease; Parkinson's disease; cancer; CD39-L4; ss.
X
S Homo sapiens.
X
X WO200110205-A1.
X
X 15-FEB-2001.
X
X 09-AUG-2000; 2000WO-US21790.
X
X 09-AUG-1999; 99US-0370265.
X
X 11-JAN-2000; 2000JS-0481238.
X
X 25-APR-2000; 2000JS-0557800.
X
X 26-MAY-2000; 2000US-0583231.
X
X 30-JUN-2000; 2000US-0608285.
X
X (HYSE-) HYSEQ INC.
X
X Ford J, Mulero JJ, Yeung G;
X
X WPI; 2001-147489/i5.
X
X P-PSDB; AAB72239.
X
X Polynucleotides encoding human CD39-like polypeptides, with apyrase
X and/or NDPase activity, which are useful in the treatment of
X pathological conditions caused by thrombosis (e.g. myocardial
X infarction) and inflammatory disorders -
X
X Claim 10; Page 156-157; 203pp; English.
X
X This invention relates to polynucleotides encoding human CD39-like
X polypeptides with apyrase and/or NDPase activity. The polypeptides having
X ATPDase, including NDPase, activity are useful for inhibiting platelet
X function and can therefore be used in the prophylaxis or treatment of
X pathological conditions caused by or involving thrombosis or excessive

CC ccagulation or excessive platelet aggregation, such as myocardial
CC infarction, cerebral ischaemia, angina, arterial thrombosis, cerebral
CC artery thrombosis or intracardiac thrombosis, and conditions associated
CC with venous thrombosis. CD39-L4 and CD39-L2 polypeptides are useful in
CC modulating disease states (including platelet aggregation, inflammation
CC and apoptosis) associated with ADP or other purinergic signalling by
CC reducing the levels of NDPs. The polypeptides are also useful for
CC prophylaxis or treatment of inflammation related disorders, such as
CC disorders involving sepsis or systemic inflammatory response syndrome or
CC SIRS (and associated conditions such as fever, tachycardia, tachypnea,
CC cytokine overstimulation); autoimmune disorders such as thrombosis,
CC atherosclerosis, acute pancreatitis, dermatitis, including psoriasis,
CC cirrhosis, reperfusion injury, asthma, multiple sclerosis, arthritis;
CC neurological disorders including neurodegenerative diseases, epilepsy,
CC depression, Alzheimer's disease, Parkinson's disease, Huntington's
CC disease, and amyotrophic lateral sclerosis; and cancer. The present
CC sequence represents cDNA encoding CD39 like protein CD39-L4.
XX
SQ Sequence 1601 BP; 436 A; 352 C; 428 G; 385 T; 0 other;

Query Match 80.3%; Score 1445; DB 22; Length 1601;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGGGCTGCCGCGCAAGGTTGGCGCGCGGCTTTTCCTTGTTCCTGTCACAAAGAAA 60
DB . . . 1 GCGGGCTGCCGCGCAAGGTTGGCGCGCGGCTTTTCCTTGTTCCTGTCACAAAGAAA 60

QY 61 TGTGGAGTGTCCTTGGCTGAATCCTCATACAGACAAGATCATTTATGGTGTGTTAGGTTGA 120
DB TGTGGAGTGTCCTTGGCTGAATCCTCATACAGACAAGATCATTTATGGTGTGTTAGGTTGA 120

QY 121 AAAAGTGATATAATAAGGAACCAAGGAGAGAAATTCAGAAAGAAATAATTCCTCT 180
DB AAAAGTGATATAATAAGGAACCAAGGAGAGAAATTCAGAAAGAAATAATTCCTCT 180

QY 181 GCAGGTGTGCGAGCAGGATTGCTTCTGCAACAAAGCCCTCCACCCAGCCACATCTTGGGA 240
DB GCAGGTGTGCGAGCAGGATTGCTTCTGCAACAAAGCCCTCCACCCAGCCACATCTTGGGA 240

QY 241 AAAGAATGGCCACTTCTTGGGGCACAGTCTTTTCATGCTGGTGTATCCTGTGTTTGA 300
DB AAAGAATGGCCACTTCTTGGGGCACAGTCTTTTCATGCTGGTGTATCCTGTGTTTGA 300

QY 301 GCGCTGTCTCCACAGGAACCAAGCAGACTTGGTTGGGGTATCTTCCTGTCTTCCATGT 360
DB GCGCTGTCTCCACAGGAACCAAGCAGACTTGGTTGGGGTATCTTCCTGTCTTCCATGT 360

QY 361 GCGCCATCAATGTCAGCCCGCAGCACCTTGTATGGAATATGTTTGTATGAGGAGCACTG 420
DB GCGCCATCAATGTCAGCCCGCAGCACCTTGTATGGAATATGTTTGTATGAGGAGCACTG 420

QY 421 GAACTCGAATTCATGTTTACACCTTTGTGCAAGAAATGCCAGGACAGCTTCCAATTCTAG 480
DB GAACTCGAATTCATGTTTACACCTTTGTGCAAGAAATGCCAGGACAGCTTCCAATTCTAG 480

QY 481 AAGGGGAAGTTTTTGTATCTGTGAAGCCAGGACTTTCTGCTTTTGTAGATCAACCTAAGC 540
DB AAGGGGAAGTTTTTGTATCTGTGAAGCCAGGACTTTCTGCTTTTGTAGATCAACCTAAGC 540

QY 541 AGGGTGTGAGACCGTTCAAGGGGCTCTTAGAGGTGGCCAAAGACTCAATCCCCCGAAGTC 600
DB AGGGTGTGAGACCGTTCAAGGGGCTCTTAGAGGTGGCCAAAGACTCAATCCCCCGAAGTC 600

QY ACTGGAAAAAGACCCCGAGTGGTCTTAAAGGCAACAGCAGGACTACGCTTACTGCCAGAAC 660
DB ACTGGAAAAAGACCCCGAGTGGTCTTAAAGGCAACAGCAGGACTACGCTTACTGCCAGAAC 660

QY 661 ACAAGCCCAAGGCTCTGCTCTTTGAGGTAAAGGAGATCTTCAGGAAGTCACCTTTCCTGG 720
DB ACAAGCCCAAGGCTCTGCTCTTTGAGGTAAAGGAGATCTTCAGGAAGTCACCTTTCCTGG 720

QY 721 TACCAAAGGGCAGTGTAGCATCATGGATGGATCCGACGAAGGCATATTAGCTTGGGTTA 780

b 721 TACCAAAGGCGAGTGTAGCATCATGGATGGATCCGACGAGGCATATTAGCTTGGGTTA 780
Y 781 CTGTGAATTTCTGACAGGTCAGCTGCATGGGCACAGACAGGAGACTGTGGGACCTTGG 840
b 781 CTGTGAATTTCTGACAGGTCAGCTGCATGGGCACAGACAGGAGACTGTGGGACCTTGG 840
Y 841 ACCTAGGGGAGCCTCCACCCAAATCACGTTTCTGCCCCAGTTTGAGAAACTCTGGAAC 900
b 841 ACCTAGGGGAGCCTCCACCCAAATCACGTTTCTGCCCCAGTTTGAGAAACTCTGGAAC 900
Y 901 AAACCTCCTAGGGCTACCTCACTTCTCTTGAGATGTTTAAACAGCACTTATAAGCTCTATA 960
b 901 AAACCTCCTAGGGCTACCTCACTTCTCTTGAGATGTTTAAACAGCACTTATAAGCTCTATA 960
Y 961 CACATAGTTACCTGGGATTTGGATTGAAAGCTGCAAGACTAGCAACCTGGGAGCCCTGG 1020
b 961 CACATAGTTACCTGGGATTTGGATTGAAAGCTGCAAGACTAGCAACCTGGGAGCCCTGG 1020
Y 1021 AGACAGAAGGGACTGATGGGCACACTTTCCGAGTGCCTGTTTACCAGATGTTTGAAG 1080
b 1021 AGACAGAAGGGACTGATGGGCACACTTTCCGAGTGCCTGTTTACCAGATGTTTGAAG 1080
Y 1081 CAGAGTGGATCTTTGGGGTGTGAAATACCACTATGTTGGCAACCAAGAGGGAGGTGG 1140
b 1081 CAGAGTGGATCTTTGGGGTGTGAAATACCACTATGTTGGCAACCAAGAGGGAGGTGG 1140
Y 1141 GCTTTGAGCCCTGCTATGCCGAAGTCTGAGGGGTGTACGAGGAAACTTCACCGCCAG 1200
b 1141 GCTTTGAGCCCTGCTATGCCGAAGTCTGAGGGGTGTACGAGGAAACTTCACCGCCAG 1200
Y 1201 AGGAGTCCAGAGAGGTTCTCTTCTATGCTTTCTTACTATTATGACCGAGCTGTTGACA 1260
b 1201 AGGAGTCCAGAGAGGTTCTCTTCTATGCTTTCTTACTATTATGACCGAGCTGTTGACA 1260
Y 1261 CAGACATGATTGATTATGAAAGGGGGGTATTTAAAGTTGAAGATTGAAGATTGAAGAAAAG 1320
b 1261 CAGACATGATTGATTATGAAAGGGGGGTATTTAAAGTTGAAGATTGAAGATTGAAGAAAAG 1320
Y 1321 CCAGGGAAGTGTGTGATAAATTGGAAACTTCACCTCAGGCAGTCCCTTCTGTGCATGG 1380
b 1321 CCAGGGAAGTGTGTGATAAATTGGAAACTTCACCTCAGGCAGTCCCTTCTGTGCATGG 1380
Y 1381 ATCTCAGCTACATACAGCCCTGTTTAAAGGATGGCTTTGGCTTTGCAGACAGCAGTCT 1440
b 1381 ATCTCAGCTACATACAGCCCTGTTTAAAGGATGGCTTTGGCTTTGCAGACAGCAGTCT 1440
Y 1441 TACAG 1445
b 1441 TACAG 1445

RESULT 7
AF63402
AAFG3402 standard; DNA; 1287 BP.

AAFG3402;

14-MAY-2001 (first entry)

Human CD39 like protein CD39-L4 coding sequence.

Human CD39-like protein: apyrase; NDPase; platelet function inhibitor;
myocardial infarction; cerebral ischaemia; angina; arterial thrombosis;
cerebral artery thrombosis; platelet aggregation; inflammation;
apoptosis; autoimmune disorder; neurological disorder;
Alzheimer's disease; Parkinson's disease; cancer; CD39-L4; ds.

Homo sapiens.

WO200110205-A1.

15-FEB-2001.

XX 09-AUG-2000; 2000WO-US21730.
PF
XX
PR 09-AUG-1999; 99US-0370265.
PR 11-JAN-2000; 2000US-0481238.
PR 25-APR-2000; 2000US-0557800.
PR 26-MAY-2000; 2000US-0583231.
PR 30-JUN-2000; 2000US-0608285.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Ford J, Mulero JJ, Yeung G;
XX
DR WPI; 2001-147489/15.
DR P-PSDB; AAB72243.
XX
PT Polynucleotides encoding human CD39-like polypeptides, with apyrase
PT and/or NDPase activity, which are useful in the treatment of
PT pathological conditions caused by thrombosis (e.g. myocardial
PT infarction) and inflammatory disorders -
XX
PS Disclosure; Page 140-142; 203pp; English.
XX
CC This invention relates to polynucleotides encoding human CD39-like
CC polypeptides with apyrase and/or NDPase activity. The polypeptides having
CC ATPDase, including NDPase, activity are useful for inhibiting platelet
CC function and can therefore be used in the prophylaxis or treatment of
CC pathological conditions caused by or involving thrombosis or excessive
CC coagulation or excessive platelet aggregation, such as myocardial
CC infarction, cerebral ischaemia, angina, arterial thrombosis, cerebral
CC artery thrombosis or intracardiac thrombosis, and conditions associated
CC with venous thrombosis. CD39-L4 and CD39-L2 polypeptides are useful in
CC modulating disease states (including platelet aggregation, inflammation
CC and apoptosis) associated with ADP or other purinergic signalling by
CC reducing the levels of NDPs. The polypeptides are also useful for
CC prophylaxis or treatment of inflammation related disorders, such as
CC disorders involving sepsis or systemic inflammatory response syndrome or
CC SIRS (and associated conditions such as fever, tachycardia, tachypnea,
CC cytokine overstimulation); autoimmune disorders such as thrombosis,
CC atherosclerosis, acute pancreatitis, dermatitis, including psoriasis,
CC cirrhosis, reperfusion injury, asthma, multiple sclerosis, arthritis;
CC neurological disorders including neurodegenerative diseases, epilepsy,
CC depression, Alzheimer's disease, Parkinson's disease, Huntington's
CC disease, and amyotrophic lateral sclerosis; and cancer. The present
CC sequence represents the CD39 like protein CD39-L4 coding sequence.
XX
SQ Sequence 1287 BP; 330 A; 290 C; 344 G; 323 T; 0 other;

Query Match 71.5%; Score 1287; DB 22; Length 1287;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1287; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 246 ATGGCCACTTCTTGGGGCACAGTCTTTTTCATGCTGGTGGTATCCTGTGTTGCGCGCT 305
Db 1 ATGGCCACTTCTTGGGGCACAGTCTTTTTCATGCTGGTGGTATCCTGTGTTGCGCGCT 60
QY 306 GTCTCCACAGGAACCCAGACACTTGGTTGAGGGGTATCTTCTGTCTTCCATGTGCCCC 365
Db 61 GTCTCCACAGGAACCCAGACACTTGGTTGAGGGGTATCTTCTGTCTTCCATGTGCCCC 120
QY 366 ATCAATGTGAGCCGACACCTTGTATGGAATATGTTTGTATGCAGGAGCACTGGAAC 425
Db 121 ATCAATGTGAGCCGACACCTTGTATGGAATATGTTTGTATGCAGGAGCACTGGAAC 180
QY 426 CGAATTCATGTTTACACCTTTGTGCAGAAAATCCAGGACAGTTCCTCAATTTCTAGAAGGG 485
Db 181 CGAATTCATGTTTACACCTTTGTGCAGAAAATCCAGGACAGTTCCTCAATTTCTAGAAGGG 240
QY 486 GAAGTTTTTGTATGTTGAAGCCAGGACTTCTCTCTTTTGTAGATCAACCTAAGCAGGGT 545
Db 241 GAAGTTTTTGTATGTTGAAGCCAGGACTTCTCTCTTTTGTAGATCAACCTAAGCAGGGT 300
QY 546 GCTGAGACCGTTCAAGGGCTCTTAGAGGTGGCCCAAGACTCAATCCCCCGGAAGTCACTGG 605

301 GCTGAGACCGTTC AAGGGCTCTTAGAGGTGGCCAAAGACTCAATCCCCGAGTCACTGG 360
606 AAAAAGACCCAGTGGTCCTAAAGGCAACAGCAGGACTTAGCGTTACTGCCAGAACACAAA 665
361 AAAAAGACCCAGTGGTCCTAAAGGCAACAGCAGGACTTAGCGTTACTGCCAGAACACAAA 420
666 GCCAAGGCTCTGCTCTTTGAGGTAAGGAGATCTTCAGGAAGTCACTTTCCTGGTACCA 725
421 GCCAAGGCTCTGCTCTTTGAGGTAAGGAGATCTTCAGGAAGTCACTTTCCTGGTACCA 480
726 AAGGGCAGTGTAGCATCATGGATGCCAGCAAGGCATATTAGCTTGGGTACTGTG 785
481 AAGGGCAGTGTAGCATCATGGATGCCAGCAAGGCATATTAGCTTGGGTACTGTG 540
786 AATTTTCTGACAGTCACTGCTGATGGCCACAGACAGGAGCTGTGGGACCTTGGACCTA 845
541 AATTTTCTGACAGTCACTGCTGATGGCCACAGACAGGAGCTGTGGGACCTTGGACCTA 600
846 GGGGGAGCCTCCACCCAAATCACGTTCCCTGCCCCAGTTTGAGAAAACCTCTGGAACAACT 905
601 GGGGGAGCCTCCACCCAAATCACGTTCCCTGCCCCAGTTTGAGAAAACCTCTGGAACAACT 660
906 CCTAGGGGCTACCTCACTTCCCTTGAGATGTTTAAACAGCACTTATAAGCTCTATACACAT 965
661 CCTAGGGGCTACCTCACTTCCCTTGAGATGTTTAAACAGCACTTATAAGCTCTATACACAT 720
966 AGTTACCTGGGATTGGATTGAAAGCTGCAAGACTAGCACACCTGGAGCCCTGGAGACA 1025
721 AGTTACCTGGGATTGGATTGAAAGCTGCAAGACTAGCACACCTGGAGCCCTGGAGACA 780
1026 GAAGGGACTGATGGGCACACTTTCCGGAGTGCCTGTTTACCGAGATGGTTGGAAGCAGAG 1085
781 GAAGGGACTGATGGGCACACTTTCCGGAGTGCCTGTTTACCGAGATGGTTGGAAGCAGAG 840
1086 TGGATCTTTGGGGTGTGAATATCCAGTATGTTGGGCAACCAAGAGGGGAGGTGGGCTTT 1145
841 TGGATCTTTGGGGTGTGAATATCCAGTATGTTGGGCAACCAAGAGGGGAGGTGGGCTTT 900
1146 GAGCCCTGCTATGCCGAAGTGTGAGGTGTACGAGGAATACTTACCAGCCAGAGGAG 1205
901 GAGCCCTGCTATGCCGAAGTGTGAGGTGTACGAGGAATACTTACCAGCCAGAGGAG 960
1206 GTCCAGAGAGGTTCCTTCTATGCTTCTCTTACTATTATGACCGAGCTGTTGACACAGAC 1265
961 GTCCAGAGAGGTTCCTTCTATGCTTCTCTTACTATTATGACCGAGCTGTTGACACAGAC 1020
1266 ATGATTGATTATGAAAAGGGGGTATTTTAAAAGTTGAAGATTTTGAAGAAGAAAGCCAGG 1325
1021 ATGATTGATTATGAAAAGGGGGTATTTTAAAAGTTGAAGATTTTGAAGAAGAAAGCCAGG 1080
1326 GAAGTGTGTATAAAGTGGAAAACCTTCACTCAGGCAGTCCCTTTCCTGTGCTATGATCTC 1385
1081 GAAGTGTGTATAAAGTGGAAAACCTTCACTCAGGCAGTCCCTTTCCTGTGCTATGATCTC 1140
1386 AGCTACATCACAGCCCTGTTTAAAGGATGGCTTTGGCTTTGCACAGACAGTCTTACAG 1445
1141 AGCTACATCACAGCCCTGTTTAAAGGATGGCTTTGGCTTTGCACAGACAGTCTTACAG 1200
1446 CTCACAAAGAAAGTGAACAACATAGAGAGGGGCTGGGCCCTTGGGGGCCACCTTTCACCTG 1505
1201 CTCACAAAGAAAGTGAACAACATAGAGAGGGGCTGGGCCCTTGGGGGCCACCTTTCACCTG 1260
1506 TTGCAGTCTCTGGGCATCTCCCATTTGA 1532
1261 TTGCAGTCTCTGGGCATCTCCCATTTGA 1287

ESULT 8
AAZ50357
D AAZ50357 standard; cDNA; 1287 BP.
X
C AAZ50357;

XX 18-MAY-2000 (first entry)
XX Human CD39-L4 variant-ACR III mutant protein encoding cDNA.
DE CD39-L4; human; apyrase; nucleotide diphosphatase; NDPase; variant;
XX ATP Diphosphohydrolase; ATPDase; adenosine diphosphate; ADP; treatment;
KW platelet aggregation; antithrombotic; thrombosis; myocardial infarction;
KW cerebral ischaemia; angina; vascular graft; extracorporeal circulation;
KW molecular weight marker; nutritional supplement; tumour; prevention;
KW drug targeting; substitution mutation; ss.
XX Homo sapiens.
OS
XX
FH Key Location/Qualifiers
FT CDS 1..1287
FT /*tag= a
FT /product= "Human CD39-L4 variant-ACR III mutant protein"
FT old_sequence replace (502..503, GA)
FT /*tag= b
FT old_sequence replace (508..510, TCC)
FT /*tag= c
FT old_sequence replace (525, A)
FT /*tag= d
XX WO2000C4041-A2.
XX 27-JAN-2000.
XX 16-JUL-1999; 99WO-US16180.
XX 16-JUL-1998; 98US-0118205.
XX 24-JUL-1998; 98US-0122449.
XX 04-FEB-1999; 99US-0244444.
XX 19-MAR-1999; 99US-0273447.
XX 09-JUL-1999; 99US-0350836.
XX (HYSE-) HYSEQ INC.
XX Ford J, Mulero J;
XX WPI; 2000-182397/16.
XX P-PSDB; AAY44850.
XX New nucleic acid encoding human CD39-like protein, useful for treating
XX and preventing thrombotic disease -
XX Example 9; Fig 6; 125pp; English.
XX The present sequence is a cDNA encoding the CD39-L4 variant, designated
XX as ACR III mutant protein, an apyrase and/or nucleotide diphosphatase
XX (NDPase). It is isolated from the human foetal liver-spleen cDNA library,
XX b2HFLS20W. It is a soluble ATP Diphosphohydrolase (ATPDase) and is
XX involved in the hydrolysis of adenosine diphosphate (ADP), the agonist
XX that causes platelet aggregation. CD39-L4 protein has 30% and 80%
XX homology to human and murine CD39. It has platelet aggregation inhibition
XX and antithrombotic activity. CD39-L4 is used to treat or prevent
XX thrombosis, myocardial infarction, cerebral ischaemia and angina. It is
XX also used in vitro, to maintain vascular grafts or during extracorporeal
XX circulation, to hydrolyse NDP, as molecular weight markers and as
XX nutritional supplements. It is used to identify therapeutic agents that
XX bind and modulate CD39-L4. It is coupled to toxins for targeting drugs
XX to tumours or other cells that express CD39-L4.
XX Sequence 1287 BP; 331 A; 291 C; 343 G; 322 T; 0 other;
SQ

Query Match 71.0%; Score 1277.4; DB 21; Length 1287;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1281; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 246 ATGGCCACTTCTTGGGGCACAGTCTTTTTCATGCTGGTGGTATCCTGTGTTGACAGCGCT 305
DB 1 ATGGCCACTTCTTGGGGCACAGTCTTTTTCATGCTGGTGGTATCCTGTGTTGACAGCGCT 60

306 GTCTCCACAGGAACGACAGACTTGGTTTGAGGGTATCTTCCTGTCTTCCATGTGCCCC 365
|||||
61 GTCTCCACAGGAACGACAGACTTGGTTTGAGGGTATCTTCCTGTCTTCCATGTGCCCC 120
|||||
366 ATCAATGTGAGCGCCAGCCCTTGATGGAATATGTTTGATGCAGGGAGCACTGGAAC 425
|||||
121 ATCAATGTGAGCGCCAGCCCTTGATGGAATATGTTTGATGCAGGGAGCACTGGAAC 180
|||||
426 CGAATTCATGTTTACACCTTTGTGCAGAAATGCCAGACAGCTTCCAAATCTAGAAGGG 485
|||||
181 CGAATTCATGTTTACACCTTTGTGCAGAAATGCCAGACAGCTTCCAAATCTAGAAGGG 240
|||||
486 GAAATTTTGTGATCTGTGAAGCCAGGACTTTCTGCTTTTGTAGATCAACCTAAGCAGGGT 545
|||||
241 GAAATTTTGTGATCTGTGAAGCCAGGACTTTCTGCTTTTGTAGATCAACCTAAGCAGGGT 300
|||||
546 GCTGAGACCGTTCAAGGGCTTTAGAGGTGGCCAAAGACTCAATCCCCCGAAGTCACTGG 605
|||||
301 GCTGAGACCGTTCAAGGGCTTTAGAGGTGGCCAAAGACTCAATCCCCCGAAGTCACTGG 360
|||||
606 AAAAAAGACCCAGTGGTCTAAAGCCAAACAGCAGGACTACGCTTACTGCCAGAACACAA 665
|||||
361 AAAAAAGACCCAGTGGTCTAAAGCCAAACAGCAGGACTACGCTTACTGCCAGAACACAA 420
|||||
666 GCCAAGGCTCTGCTCTTTGAGTAAAGGAGATCTTTCAGAAAGTCACCTTTCTCGGTACCA 725
|||||
421 GCCAAGGCTCTGCTCTTTGAGTAAAGGAGATCTTTCAGAAAGTCACCTTTCTCGGTACCA 480
|||||
726 AAGGGCAGTGTAGCATCATGGATCGACGAGGATATAGCTTGGGTTACTGTG 785
|||||
481 AAGGGCAGTGTAGCATCATGGATCGACGAGGATATAGCTTGGGTTACTGTG 540
|||||
786 AATTTTCTGACAGGTCAGCTGATGGCCACAGACAGAGACTGTGGGACCTTGGACCTA 845
|||||
541 AATTTTCTGACAGGTCAGCTGATGGCCACAGACAGAGACTGTGGGACCTTGGACCTA 600
|||||
846 GGGGAGCCTCCACCCAAATCAGCTTCCCTGCCCCAGTTTGAGAAACTCTGGAACAAACT 905
|||||
601 GGGGAGCCTCCACCCAAATCAGCTTCCCTGCCCCAGTTTGAGAAACTCTGGAACAAACT 660
|||||
906 CCTAGGGGCTACCTCACTTCTTTGAGATGTTTAAACAGCACTTATAAGCTCTATACACAT 965
|||||
661 CCTAGGGGCTACCTCACTTCTTTGAGATGTTTAAACAGCACTTATAAGCTCTATACACAT 720
|||||
966 AGTTACCTGGGATTTGGATTGAAAGCTGCAAGACTAGCAACCCCTGGGAGCCCTGGAGACA 1025
|||||
721 AGTTACCTGGGATTTGGATTGAAAGCTGCAAGACTAGCAACCCCTGGGAGCCCTGGAGACA 780
|||||
1026 GAAGGAGCTGATGGGCACACTTCCGGAGTGCCTGTTTACCGAGATGGTTGGAAGCAGAG 1085
|||||
781 GAAGGAGCTGATGGGCACACTTCCGGAGTGCCTGTTTACCGAGATGGTTGGAAGCAGAG 840
|||||
1086 TGSATCTTTGGGGGTGTGAATACCACTATGGTGGCAACCAAGAGGGGAGGTGGGCTTT 1145
|||||
841 TGSATCTTTGGGGGTGTGAATACCACTATGGTGGCAACCAAGAGGGGAGGTGGGCTTT 900
|||||
1146 GAGCCTGCTATGCCGAAGTGTGAGGGTGGTACGAGAAACTTCAACCAGCAGAGGAG 1205
|||||
901 GAGCCTGCTATGCCGAAGTGTGAGGGTGGTACGAGAAACTTCAACCAGCAGAGGAG 960
|||||
1206 GTCCAGAGAGGTTCTCTTATGCTTCTCTTACTATTATGACCGAGCTGTTGACACAGAC 1265
|||||
961 GTCCAGAGAGGTTCTCTTATGCTTCTCTTACTATTATGACCGAGCTGTTGACACAGAC 1020
|||||
1266 ATGATTGATTATGAAAAGGGGGGTATTTTAAAGTTGAAGATTTTGAAGAAAGCCAGG 1325
|||||
1021 ATGATTGATTATGAAAAGGGGGGTATTTTAAAGTTGAAGATTTTGAAGAAAGCCAGG 1080
|||||
1326 GAAGTGTGTATAACTTGGAAACTTCAACCTCAGGCAGTCTTCTTCTGTGCATGGATCTC 1385
|||||
1081 GAAGTGTGTATAACTTGGAAACTTCAACCTCAGGCAGTCTTCTTCTGTGCATGGATCTC 1140
|||||

QY 1386 AGCTACATCACAGCCCTGTAAAGGATGGCTTTGGCTTTGCAGACAGCACAGTCTTACAG 1445
|||||
Db 1141 AGCTACATCACAGCCCTGTAAAGGATGGCTTTGGCTTTGCAGACAGCACAGTCTTACAG 1200
|||||
QY 1446 CTCACAAAGAAAGTGAACAAACATAGAGACGGGCTGGGCTTGGGGCCACCTTTACCTG 1505
|||||
Db 1201 CTCACAAAGAAAGTGAACAAACATAGAGACGGGCTGGGCTTGGGGCCACCTTTACCTG 1260
|||||
QY 1506 TTGCAGTCTCTGGGCATCTCCCATTTGA 1532
|||||
Db 1261 TTGCAGTCTCTGGGCATCTCCCATTTGA 1287
|||||
RESULT 9
AAF63385
ID AAF63385 standard; DNA; 1287 BP.
AC AAF63385;
XX
DT 14-MAY-2001 (first entry)
XX
DE DNA encoding human CD39 like protein CD39-L4 variant ACR111.
XX
KW Human CD39-like protein; apyrase; NDPase; platelet function inhibitor;
KW myocardial infarction; cerebral ischaemia; angina; arterial thrombosis;
KW cerebral artery thrombosis; platelet aggregation; inflammation;
KW apoptosis; autoimmune disorder; neurological disorder; mutant;
KW Alzheimer's disease; Parkinson's disease; cancer; CD39-L4; ds.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WC200110205-A1.
XX
PD 15-FEB-2001.
XX
PF 09-AUG-2000; 2000WO-US21790.
XX
PR 09-AUG-1999; 99US-0370265.
PR 11-JAN-2000; 2000US-0481238.
PR 25-APR-2000; 2000US-0557800.
PR 26-MAY-2000; 2000US-0583231.
PR 30-JUN-2000; 2000US-0608285.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Ford J, Mulero JJ, Yeung G;
XX
DR WP1; 2001-147489/15.
DR P-PSDB; AAB72240.
XX
PT Polynucleotides encoding human CD39-like polypeptides, with apyrase
PT and/or NDPase activity, which are useful in the treatment of
PT pathological conditions caused by thrombosis (e.g. myocardial
PT infarction) and inflammatory disorders -
XX
PS Example 9; Fig 6; 203pp; English.
XX
CC This invention relates to polynucleotides encoding human CD39-like
CC polypeptides with apyrase and/or NDPase activity. The polypeptides having
CC ATPase, including NDPase, activity are useful for inhibiting platelet
CC function and can therefore be used in the prophylaxis or treatment of
CC pathological conditions caused by or involving thrombosis or excessive
CC coagulation or excessive platelet aggregation, such as myocardial
CC infarction, cerebral ischaemia, angina, arterial thrombosis, cerebral
CC artery thrombosis or intracardiac thrombosis, and conditions associated
CC with venous thrombosis. CD39-L4 and CD39-L2 polypeptides are useful in
CC modulating disease states (including platelet aggregation, inflammation
CC and apoptosis) associated with ADP or other purinergic signalling by
CC reducing the levels of NDPs. The polypeptides are also useful for
CC prophylaxis or treatment of inflammation related disorders, such as
CC disorders involving sepsis or systemic inflammatory response syndrome or
CC SIRS (and associated conditions such as fever, tachycardia, tachypnea,

cytokine overstimulation); autoimmune disorders such as thrombosis, atherosclerosis, acute pancreatitis, dermatitis, including psoriasis, cirrhosis, reperfusion injury, asthma, multiple sclerosis, arthritis; neurological disorders including neurodegenerative diseases, epilepsy, depression, Alzheimer's disease, Parkinson's disease, Huntington's disease, and amyotrophic lateral sclerosis; and cancer. The present sequence represents DNA encoding variant ACRIII of human CD39 like protein CD39-L4.

Sequence 1287 BP; 331 A; 291 C; 343 G; 322 T; 0 other;

Query Match 71.0%; Score 1277.4; DB 22; Length 1287;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1281; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

246 ATGGCCACTTCTTGGGGCACAGTCTTTTTCATGCTGGTGGTATCCTTTCATGTCGCT 305
1 ATGGCCACTTCTTGGGGCACAGTCTTTTTCATGCTGGTGGTATCCTTTCATGTCGCT 60

306 GTCTCCACAGGAACACAGACCTTGGTTTGAGGGTATCTTCCCTGCTTCCATGTGCCCC 365
61 GTCTCCACAGGAACACAGACCTTGGTTTGAGGGTATCTTCCCTGCTTCCATGTGCCCC 120

366 ATCAATGTCAGCGCCAGCACCTTGTATGGAATTATGTTGATCAGGGAGCACTGGAAC 425
121 ATCAATGTCAGCGCCAGCACCTTGTATGGAATTATGTTGATCAGGGAGCACTGGAAC 180

426 CGAATTGATGTTACACCTTGTGCGAGAAATGCCAGGACAGCTTCCAATCTAGAAGGG 485
181 CGAATTGATGTTACACCTTGTGCGAGAAATGCCAGGACAGCTTCCAATCTAGAAGGG 240

486 GAAGTTTGTGTTGAAGCCAGGACTTCTGCTTTTGTAGATCAACCTAAGCAGGGT 545
241 GAAGTTTGTGTTGAAGCCAGGACTTCTGCTTTTGTAGATCAACCTAAGCAGGGT 300

546 GCTGAGACCGTTCAGGGCTCTTAGAGGTGGCCAAAGACTCAATCCCCCGAAGTCACTGG 605
301 GCTGAGACCGTTCAGGGCTCTTAGAGGTGGCCAAAGACTCAATCCCCCGAAGTCACTGG 360

606 AAAAAGACCCAGTGTCTTAAGGCAACAGCAGGACTACGGTTACTGCCAGAACACAA 565
361 AAAAAGACCCAGTGTCTTAAGGCAACAGCAGGACTACGGTTACTGCCAGAACACAA 420

666 GCCAAGGCTCTGCTTTGAGGTAAAGGAGATCTTCAGGAAGTCACTTCCCTGGTACCA 725
421 GCCAAGGCTCTGCTTTGAGGTAAAGGAGATCTTCAGGAAGTCACTTCCCTGGTACCA 480

726 AAGGGCAGTGTAGCATCATGGATGGATCCGACGAAGGCATATTAGCTTGGTTACTGTG 785
481 AAGGGCAGTGTAGCATCATGGATGGACAGACGAAGGCATATTGCTTGGTTACTGTG 540

786 AATTTTCTGACAGGTGAGTGCATGGCCACAGACAGGAGACTGTGGGACCTTGGACCTA 845
541 AATTTTCTGACAGGTGAGTGCATGGCCACAGACAGGAGACTGTGGGACCTTGGACCTA 600

846 GGGGAGCCTCCACCAAAATCACGTTCTGCCCCAGTTTGAGAAACTCTGGAACAACT 905
601 GGGGAGCCTCCACCAAAATCACGTTCTGCCCCAGTTTGAGAAACTCTGGAACAACT 660

906 CCTAGGGCTACCTTCACTTCTCTTTGAGATGTTTAAACAGCACTTATAAGCTCTATACAT 965
661 CCTAGGGCTACCTTCACTTCTCTTTGAGATGTTTAAACAGCACTTATAAGCTCTATACAT 720

966 AGTTACCTGGGATTTGGAATTGAAGCTGCAAGACTAGCAACCTGGGAGCCCTGGAGACA 1025
721 AGTTACCTGGGATTTGGAATTGAAGCTGCAAGACTAGCAACCTGGGAGCCCTGGAGACA 780

1026 GAAGGGACTGATGGGCACACTTTCGGAGTGCCTTTTACCGAGATGGTTGGAAGCAGAG 1085
781 GAAGGGACTGATGGGCACACTTTCGGAGTGCCTTTTACCGAGATGGTTGGAAGCAGAG 840

1086 TGGATCTTGGGGTGTGAAATACCAAGTATGGTGGCAACCAAGAGGGGAGGTGGGCTTT 1145

841 TGGATCTTTGGGGTGTGAAATACCAAGTATGGTGGCAACCAAGAGGGAGGTGGGCTTT 900

1146 GAGCCTGCTATGCCGAAGTCTGAGGGTGTACAGSAGAAAACCTTCACCGACAGAGGAG 1205

901 GAGCCTGCTATGCCGAAGTCTGAGGGTGTACAGSAGAAAACCTTCACCGACAGAGGAG 960

1206 GTCCAGAGAGGTTCCCTTCTATGCTTTCTCTTACTATTATGACCGAGCTGTGACACAGAC 1265

961 GTCCAGAGAGGTTCCCTTCTATGCTTTCTCTTACTATTATGACCGAGCTGTGACACAGAC 1020

1266 ATGATTGATTATGAAAAGGGGGTATTTTAAAAGTTGAAGATTTTGAAGAAAAGCCAGG 1325

1021 ATGATTGATTATGAAAAGGGGGTATTTTAAAAGTTGAAGATTTTGAAGAAAAGCCAGG 1080

1326 GAAGTCTGTGATAACTTTGAAAAACTTCACCTCAGGCAGTCTTTCCCTGTGCATGGATCTC 1385

1081 GAAGTCTGTGATAACTTTGAAAAACTTCACCTCAGGCAGTCTTTCCCTGTGCATGGATCTC 1140

1386 AGCTACATCACAGCCCTGTAAAGGATGGCTTTGGCTTTGCAGACAGCAGTCTTACAG 1445

1141 AGCTACATCACAGCCCTGTAAAGGATGGCTTTGGCTTTGCAGACAGCAGTCTTACAG 1200

1446 CTCAAAAGAAAGTGAACAACATAGAGACGGCTGGGCCCTTGGGGGCCACCTTTTACCTG 1505

1201 CTCAAAAGAAAGTGAACAACATAGAGACGGCTGGGCCCTTGGGGGCCACCTTTTACCTG 1260

1506 TTGCAGTCTCTGGGCATCTCCCAATTGA 1532

1261 TTGCAGTCTCTGGGCATCTCCCAATTGA 1287

RESULT 10
AAC98093
ID AAC98093 standard; cDNA; 1457 BP.
XX
AC AAC98093;
XX
DT 39-MAR-2001 (first entry)
XX
DE Human colon cancer antigen nucleotide sequence SEQ ID NO:103.
XX
KW Human; colon cancer; colon cancer antigen; diagnosis; detection; identification; cytostatic; cardioactive; neuroprotective; vulnery;
KW immunomodulatory; muscular; gynaecological; gastrointestinal;
KW nephrotropic; anti-infective; antibacterial; gene therapy; wound;
KW neural disorder; immune system disorder; muscular disorder;
KW reproductive disorder; gastrointestinal disorder; renal disorder;
XX infectious disease; cardiovascular disorder; ss.
OS Homo sapiens.
XX
XX MO200055351-A1.
PN
XX
PD 21-SEP-2000.
XX
PF 08-MAR-2000; 2000WO-US05883.
XX
PR 12-MAR-1999; 99US-0124270.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
DR WPI; 2000-587534/55.
DR P-PSDB; AAB53336.
XX
PT Colon cancer associated gene sequences, referred to as colon cancer
PT antigens, useful for the treatment, prevention, and diagnosis of colon
PT disorders such as colon cancer -
XX
PS Claim 1; Page 544; 2104pp; English.
XX AAC97991 to AAC98763 encode the human colon cancer associated proteins.
CC

C called human colon cancer antigens, given in AAB53234 to AAB54006. The
C human colon cancer antigens can have cytostatic, cardioactive, muscular;
C neuroprotective, immunomodulatory, gynaecological, gastrointestinal,
C vulnery, nephrotropic, antiinfective and antibacterial activities, and
C can be used in gene therapy. The colon cancer antigen polynucleotides,
C proteins and antibodies to the proteins are useful for the prevention,
C treatment and diagnosis of colon disorders, such as colon cancer. The
C polynucleotides may be used in diagnostics and research. The as for
C chromosome identification, and as hybridisation probes. The proteins
C may also be used to prevent diseases such as neural disorders, immune
C system disorders, muscular disorders, reproductive disorders,
C gastrointestinal disorders, wounds, renal disorders, infectious
C diseases, and cardiovascular disorders. AAC98764 to AAC98772 and
C AAB54007 represent sequences used in the exemplification of the present
C invention.

X Q Sequence 1457 BP; 408 A; 338 C; 350 G; 354 T; 7 other;

Query Match 60.5%; Score 1089.2; DB 2i; Length 1457;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 1085; Conservative 9; Mismatches 2; Indels 0; Gaps 0;

y 553 CCGTCAAGGGCTCTTAGAGGTGGCCAAAGACTCAATCCCCGAAAGTCACTGGAAGAAAGA 612
b 14 CCGTCAAGGGCTCTTAGAGGTGGCCAAAGACTCAATCCCCGAAAGTCACTGGAAGAAAGA 73
y 613 CCCCAGTGGTCTTAAGGCAACAGCAGGACTACGCTTACTGCCAGAACACAAAGCCRAAG 672
b 74 CCCCAGTGGTCTTAAGGCAACAGCAGGACTACGCTTACTGCCAGAACACAAAGCCRAAG 133
y 673 CTCTGCTCTTTGAGGTAAGGAGATCTTCAGGAAGTCACCTTTCCCTGGTACCAAGGGCA 732
b 134 CTCTGCTCTTTGAGGTAAGGAGATCTTCAGGAAGTCACCTTTCCCTGGTACCAAGGGCA 193
y 733 GTGTAGCATCATGGATGGATCCGACGAAGGCATATTAGCTTGGGTTACTCTGAATTTTC 792
b 194 GTGTAGCATCATGGATGGATCCGACGAAGGCATATTAGCTTGGGTTACTCTGAATTTTC 253
y 793 TGACAGGTCAGCTGCATGGCCACAGACAGGAGACTCTGGGGACCTTGGACCTAGGGGGAG 852
b 254 TGACAGGTCAGCTGCATGGCCACAGACAGGAGACTCTGGGGACCTTGGACCTAGGGGGAG 313
y 853 CTTCCACCCCAATCACGTTCTCTGCCCCAGTTTGAGAAACTCTGGAACAACTCCTAGGG 912
b 314 CTTYCACCCCAATCACGTTCTCTGCCCCAGTTTGAGAAACTCTGGAACAACTCCTAKGG 373
y 913 GCTACCTCACTTCTCTTGAGATGTTTAAACAGCATTATTAAGCTCTATACATAGTTACC 972
b 374 GCTACCTCACTTCTCTTGAGATGTTTAAACAGCATTATTAAGCTCTATACATAGTTACT 433
y 973 TGGGATTTGGATTGAAAGCTGCAAGACTAGCAACCTCGGAGCCCTGGAGACAGAGGGA 1032
b 434 TGGGATTTGGATTGAAAGCTGCAAGACTAGCAACCTCGGAGCCCTGGAGACAGAGGGA 493
y 1033 CTGATGGGCACACTTTCGGGAGTGCCCTGTTTACCGAGATGCTTGGAGCAGAGTGSATCT 1092
b 494 CTGATGGGCACACTTTCGGGAGTGCCCTGTTTACCGAGATGCTTGGAGCAGAGTGSATCT 553
y 1093 TTGGGGGTGTGAAATACCAAGTATGGTGGCAACCAAGAGGGGAGGTGGGCTTGAAGCCCT 1152
b 554 TTGGGGGTGTGAAATACCAAGTATGGTGGCAACCAAGAGGGGAGGTGGGCTTGAAGCCCT 613
y 1153 GCTATGCCGAAGTGCTGAGGGTGGTACGAGGAAACCTTACCAGCCAGAGGAGGTCCAGA 1212
b 614 GCTATGCCGAAGTGCTGAGGGTGGTACGAGGAAACCTTACCAGCCAGAGGAGGTCCAGA 673
y 1213 GAGGTTCTCTATGCTTTCTCTTACTATTATGACCGAGCTGTTGACACAGACATGATTG 1272
b 674 GAGGTTCTCTATGCTTTCTCTTACTATTATGACCGAGCTGTTGACACAGACATGATTG 733
y 1273 ATTATGAAAGGGGGTATTTTAAAGTTGAAGATTTTGAAGAAAGCCAGGAAAGTGT 1332
b 734 ATTATGAAAGGGGGTATTTTAAAGTTGAAGATTTTGAAGAAAGCCAGGAAAGTGT 793

Qy 1333 GTGATAACTTGGAAAACTTCACCTCAGGCAGTCCTTTTCTGTGATGGATCTCAGCTACA 1392
Db 794 GTGATAACTTGGAAAACTTCACCTCAGGCAGTCCTTTTCTGTGATGGATCTCAGCTACA 853
Qy 1393 TCACAGCCCTGTAAAGGATGGCTTTGGCTTTGCAGACAGCAGTCTTTACAGCTCACA 1452
Db 854 TCACAGCCCTGTAAAGGATGGCTTTGGCTTTGCAGACAGCAGTCTTTACAGCTCACA 913
Qy 1453 AGAAAGTGAACACATAGAGACGGGCTGGGCTTGGGGCCACCTTTACCTGTTGCAGT 1512
Db 914 AGAAAGTGAACACATAGAGACGGGCTGGGCTTGGGGCCACCTTTACCTGTTGCAGT 973
Qy 1513 CTCTGGGCATCTCCCATTTAGGACGCTTCTGAACTAGTCTGGAGACCTTGCACACCT 1572
Db 974 CTCTGGGCATCTCCCATTTAGGACGCTTCTGAACTAGTCTGGAGACCTTGCACACCT 1633
Qy 1573 TTTTAAGGGGAGAGAGACACTTAGTTTCTGAACTAGTCTGGGACATCTGGACTTGA 1632
Db 1034 TTTTAAGGGGAGAGAGACACTTAGTTTCTGAACTAGTCTGGGACATCTGGACTTGA 1693
Qy 1633 GCCTAGAGATTWGT 1648
Db 1094 GCCTAGAGATTAGGT 1109

RESULT 11

AAD31696

ID AAD31696 standard; cDNA; 2119 BP.

XX AAD31696;

DT 18-JUN-2002 (first entry)

XX Mouse CD39L4 CDNA.

Mus musculus.
Key Location/Qualifiers
CDS 205..1602
/*tag= a
/product= "Mouse CD39L4 protein"
US6350447-B1.
26-FEB-2002.
29-JAN-1999; 99US-0240639.
29-JAN-1999; 99US-0240639.
(HYSE-) HYSEQ INC.
Chadwick BP, Frischau A;
WPI; 2002-215262/27.
P-PSDB; AAE19884.
An isolated polypeptide with phosphohydrolase activity, designated
CD39L2, useful to identify other proteins with which binding occurs or

Mus musculus.

Key Location/Qualifiers

CDS 205..1602

/*tag= a

/product= "Mouse CD39L4 protein"

US6350447-B1.

26-FEB-2002.

29-JAN-1999; 99US-0240639.

29-JAN-1999; 99US-0240639.

(HYSE-) HYSEQ INC.

Chadwick BP, Frischau A;

WPI; 2002-215262/27.

P-PSDB; AAE19884.

An isolated polypeptide with phosphohydrolase activity, designated
CD39L2, useful to identify other proteins with which binding occurs or

T identify inhibitors and for treatment of, e.g., Alzheimer's, multiple
T sclerosis and osteoporosis -
X
S Example; Fig 1; 101pp; English.

X The present invention relates to novel proteins with phosphohydrolase
C activity, designated CD-39-like (CD39L) proteins and polynucleotides
C encoding such proteins. CD39L proteins are useful to treat infectious
C diseases caused by viral, bacterial, fungal or other infection that may
C be treatable with CD39L. They are useful in the treatment of various
C immune deficiencies and disorders, autoimmune disorders such as multiple
C sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune
C thyroiditis and insulin dependent diabetes mellitus, allergic reactions
C and conditions such as asthma and other respiratory problems, periodontal
C disease, osteoporosis, osteoarthritis and other tooth repair processes.
C They may have utility in compositions used for bone, cartilage, tendon,
C ligament and/or nerve tissue growth or regeneration as well as for wound
C healing and tissue repair and replacement and in the treatment of burns,
C incisions and ulcers. CD39L proteins may also be useful for proliferation
C of neural cells and for regeneration of nerve and brain tissue, i.e. for
C the treatment of central nervous system diseases such as Alzheimer's
C disease, Parkinson's disease, amyotrophic lateral sclerosis, Huntington's
C disease, peripheral nervous system diseases peripheral nerve injuries,
C peripheral neuropathy and localised neuropathies. They are also used to
C treat mechanical and traumatic disorders which involve degeneration,
C death or trauma to neural cells or nerve tissue. CD39L proteins of the
C invention are also useful to promote better or faster closure of non-
C healing wounds, including pressure ulcers, ulcers associated with
C vascular insufficiency and surgical and traumatic wounds. They also
C exhibit anti-inflammatory activity and may be used to treat inflammatory
C conditions including chronic or acute conditions), including ischaemia-
C reperfusion injury, endotoxin lethality, arthritis, nephritis, cytokine
C or chemokine-induced lung injury, inflammatory bowel disease or Crohn's
C disease. The present sequence is a DNA encoding mouse CD39L4 protein,
C also known as nucleotide-triphosphatase (NTPase). CD39L4 gene is
C localised on chromosome 12.

X Sequence 2119 BP; 545 A; 482 C; 546 G; 546 T; 0 other;

Query Match		58.3%;	Score 1049.6;	DB 24;	Length 2119;
Best Local Similarity		81.4%;	Pred. No. 0;		
Matches 1270;		Conservative	0;	Mismatches	274;
				Indels	16;
				Gaps	4;
Y	48	GTCACAAAGAAATGTGGAGTGTCTGGCTGAATCCTCATACAGACAAGATCATTA----	103		
b	3	GTTGACACAGGAATGAAGAGTGTATTGGCTGMACTCTTCACAGCAGAGCGGATATTGACCAT	62		
Y	124	----TGGTGTGTAGGTTGAAAAAGTGATATAATAAAGGAACCAAGAGAAAAATTCAGA	159		
b	63	GTGCTTTTAAATGGCCCTGCGTGACCCGCCACCTTGCTGTAAAGAAGAACCGGCCAA	122		
Y	160	AGGAAGAAAAAATTCCTCTGCAGGTGTGCGAGCAGGATTCCTTCTGCAACAAAGCCT	219		
b	123	GGGAGGCGCTGAAGGACCTCCACAGGAGTGTGAGCAGCACCTGCTTCAGCAACAAG----	178		
Y	220	CCACCCAGCCACATCTTGGGAAAAAGAAATGGCCACTTCTTGGGGCACAGTCTTTTTCATGC	279		
b	179	CCTCAGGTCCACATCTTGGGAAGAAATATGGCCACTTCCCTGGGGGCTGTC---TTCATGC	235		
Y	280	TGGTGGTATCCCTGTGTTGACGGCTGTCTCCACAGGAACCCAGCAGACTTGTGTTGAGG	339		
b	236	TGATCATAGCCTCGCTGGCAGCACTGTCTCTACAGAGAACAGCAGACCTGTTTGAAG	295		
Y	340	GTATCTTCCTGTCTCCATGTGCCCCCATCAATGTCTCAGCGCCAGCACCTTGTATGGAAATTA	399		
b	296	GTGCTCTCTTGTCTCCATGTGCCCCCATTAATGTCTCAGTGCCGCGCACCTTTTATGGAAATTA	355		
Y	400	TGTTTGATGCAGGAGCAGCTGGAACCTCGAATTCATGTTTACACCTTTGTGCAGAAATGC	459		
b	356	TGTTTGATGCGGCGCAGCAGCTGGAGCTCGGATTCATGTTTACACTTTTGTGCAGAAACAG	415		
Y	460	CAGGACAGCTTCCAAATTTAGAAGGGGAAGTTTTTGATTTCTGTGAAGCCAGGACTTTCTG	519		

Db	416	CAGGACAGCTCCCTTTCTGTGAAGGTGAAATTTTGATTTCTGTGAAGCCGGGACTTTCTG	475
Qy	520	CTTTGTAGATCAACCTTAAGCAGGGTGTCTGAGACGGTTCAAGGGCTTTAGAGGTGGCCA	579
Db	476	CTTTGTGGATCAGCCCAACACAGGGTGTCTGAGACTGTCTCAGGAGCTCTTGAGGTGSCCA	535
Qy	580	AAGACTCAATCCCCGAGTCACTGGAAAAAGACCCAGTGGTCTCTAAAGGCAACAGCAG	639
Db	536	AAGACTCGATCCCCAGAGCCACTGGGAAAGGACCCCGTGGTTCTGAAAGCAACGGCCG	595
Qy	640	GACTACGCTTACTGCCAGAACACAAAGCCAAAGGCTCTGCTCTTTGAGSTAAAGGAGATCT	699
Db	596	GACTCCGTTTGTCTGCTGAGCAGAAAGCCAGGCTCTGCTCTTTGGAGGTAGAGGAGATCT	655
Qy	700	TCAGGAAGTCACCTTTCCTGGTACCAAAGGGCAGTGTGTAGCATCATGGATGGATCCGACG	759
Db	656	TCAGAATTCACCTTTCCTGGTCCAGATGGCAGCTGTAGCATCATGGATGGTCTCTATG	715
Qy	760	AAGGCATATTAGCTTGGGTTACTGTGAATTTTCTGACAGGTCAGCTGCATGGCCACAGAC	819
Db	716	AAGGCATACTAGCTGGGTGTACCGTGAACCTTTCTAACAGGTCAGCTGCATGGTCTGTGCC	775
Qy	820	AGGAGACTGTGGGACCTTGGACCTAGGGGGAGGCTCCACCCAAATCACGTTCTCTGCCCC	879
Db	776	AGGAGACTGTGGGACCTTGGACCTGGGGGTGCTCCACCCAAATCACGTTCTACCCC	835
Qy	880	AGTTTGAGAAAACTCTGGAAACAACTCCTAGGGGTACCTCACCTTCCTTTGAGATGTTTA	939
Db	836	AGTTTGAGAAAACTCTGGAAACAACTCCTAGGGGTACCTCACCTTCCTTTGAGATGTTTA	895
Qy	940	ACAGCACTTATAAGCTCTATACATAGTTTACCTGGGATTTGGATTGAAGCTTCAAGAC	999
Db	896	ACAGCACTTTTAAAGCTCTATACATAGTTTACTTGGGATTTGGACTGAAGCTGCAAGAC	955
Qy	1000	TAGCAACCTTGGAGCCCTGGAGACAGAAGGGAGTGTATGGGCACACTTTCCGGAGTGCCT	1059
Db	956	TGGCAACTCTGGGAGCCCTGGAAAGCAAAAGGGACTGTATGGACATACGTTTCGAAAGTGCCT	1015
Qy	1060	GTTTACCGAGATGGTTGGAAGCAGAGTGGATCTTTGGGGGTGTGAAATACCAAGTATGGTG	1119
Db	1016	GTTTACCAAGATGGTTGGAAGCAGAGTGGATCTTTGGSGGTGTGAAATACCAAGTATGGTG	1075
Qy	1120	GCAACCAAGAGGGGAGGTGGGCTTTGAGCCCTGCTATGCCGAAGTGTGAGGGGTGTAC	1179
Db	1076	GTAACCAAGAGGGGAGATGGCTTTGAACCTGCTATGCGGAAGTGTGAGGGTAGTAC	1135
Qy	1180	GAGGAAAACTTCACAGCCAGAGGAGGTCCAGAGAGGTTTCTTCTATGCTTCTTCTTACT	1239
Db	1136	AGGGAAAACTTCACAGCCAGAGAGTCCGAGGAAGTCCGAGGAAGGCTTCTACGCTTCTTACT	1195
Qy	1240	ATTATGACCGAGCTGTTGACACAGACATGATTGATGATGAAAGGGGGGTATTTAAAG	1299
Db	1196	ACTACGATCGAGCGCTGACACACACTTGATCGATTATGAAAGGGCGGGTTTAAAG	1255
Qy	1300	TTGAAGATTTTGAAGAAAGCCAGGAGTGTGTGATACCTTGGAAACCTTCACCTCAG	1359
Db	1256	TTGAAGATTTTGAAGAAAGCCAGAGAGTGTGTGACAACTTGGGGAGCTTCTCCTCGG	1315
Qy	1360	GCAGTCTTCTCTGTCATGGATCTCAGCTACATCACAGCCCTGTGTTAAAGGATGGCTTG	1419
Db	1316	GCAGTCTTCTCTGTCATGGACCTCATTACATCACAGCCCTGTTGAAAGATGGTTTG	1375
Qy	1420	GCTTTGTCAG-ACAGCAGTCTTTACAGCTCACAAAGAAAGTGAACACATAGAGACGGGC	1478
Db	1376	GCTTTGCCGAACGGCACCTCTTACAGCTCACAAAGAAAGTGAACACATAGAGACTGGT	1435
Qy	1479	TGGCCCTTGGGGCCACCTTTACCTGTTGAGTCTCTGGGCATCTCCCATTTGAGGCCAC	1538
Db	1436	TGGCCCTTGGGGCCACCTTTACCTGCTCCAGTCTCTGGGCATCACCCAGCTGAGGCCAA	1495
Qy	1539	GTACTTCTCTTGGAGACCTGCAATTTGCCAACACCTTTTAAAGGGGAGGAGAGACACTTAG	1598
Db	1496	GCTCCACCTCTGAAGCCTGCAATTTCTGAACCACTTTCTCACAGGAAGGCGCTGGACTCAG	1555

401 GTTTGATGCAGGAGCACTGGAATTCATGTTACACCTTTGTGCGAGAAATGCC 460

C patient;
C (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
X
Q Sequence 488 BP; 114 A; 107 C; 124 G; 143 T; 0 other;
Query Match 20.2%; Score 363.4; DB 23; Length 488;
Best Local Similarity 91.5%; Pred. No. 2.2e-102;
Matches 396; Conservative 0; Mismatches 36; Indels 1; Gaps 1;
Y 117 TTGAAAAGTGATATATAAAGGAACCAAGGAGAAAATTCAGAGGAAGAAAATTC 176
b 57 TTTTACAGGTGTAACCTAAAAGCTAGTTGGTCTTAACCTTGTGTCTTTGTCTTATAAGC 116
Y 177 CTCTGCAGGTGTGCGAGCAGGATTGCTTCTGCAACAAGAGCTCCACCCAGCCACATCTT 236
b 117 CTCTGCAGGTGTGCGAGCAGGATTGC-TCTGCAACAAGAGCTCCACCCAGCCACATCTT 175
Y 237 GGGAAAAGATGGCCACTTCTTGGGGCACAGTCTTTTTCATGTGCTGGTGGTATCCTGTGTT 296
b 176 GGGAAAAGATGGCCACTTCTTGGGGCACAGTCTTTTTCATGTGCTGGTGGTATCCTGTGTT 235
Y 297 TGCAGCGCTGTCTCCACAGGAACCAAGCAGACCTTGGTTGAGGGTATCTTCCGTCTTCC 356
b 236 TGCAGCGCTGTCTCCACAGGAACCAAGCAGACCTTGGTTGAGGGTATCTTCCGTCTTCC 295
Y 357 ATGTGCCCCATCAATGTGCGCCAGCAGCACCTTGTATGGAATTATGTTGATGCGAGGAGC 416
b 296 ATGTGCCCCATCAATGTGCGCCAGCAGCACCTTGTATGGAATTATGTTGATGCGAGGAGC 355
Y 417 ACTGGAACCTCGAATTCATGTTTACACCTTTGTGCAAGAAATGCCAGGACAGCTTCCAAAT 476
b 356 ACTGGAACCTCGAATTCATGTTTACACCTTTGTGCAAGAAATGCCAGGACAGCTTCCAAAT 415
Y 477 CTAGAAGGGGAAGTTTTTGAATCTGTGAAGCCAGGACTTTCTGCTTTTGTAGATCAACCT 536
b 416 CTAGAAGGGGAAGTTTTTGAATCTGTGAAGCCAGGACTTTCTGCTTTTGTAGATCAACCT 475
Y 537 AAGCAGGCTGCTG 549
b 476 AAGCAGGCTGCTG 488
RESULT 14
BV22567
D ABV22567 standard; cDNA; 480 BP.
X
X C ABV22567;
X T 13-SEP-2002 (first entry)
X Human prostate expression marker cDNA 22558.
E Human prostate expression marker cDNA 22558.
W Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
W pharmacogenomic marker; gene; ss.
X Homo sapiens.
S WO200160860-A2.
X
X D 23-AUG-2001.
X F 20-FEB-2001; 2001WO-US05171.
X R 17-FEB-2000; 2000US-183319P.
R 16-MAR-2000; 2000US-189862P.
R 25-MAY-2000; 2000US-207454P.
R 09-JUN-2000; 2000US-211314P.
R 18-JUL-2000; 2000US-219007P.
R 13-DEC-2000; 2000US-255281P.
X
X (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
A Schlegel R, Endege WO, Monahan JE;
X I

XX WPI; 2001-662795/76.
XX Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer -
PS Claim 1; Page 3945; 11750pp; English.
XX The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABVCC010-ABV62213) of the specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a patient;
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX Sequence 480 BP; 111 A; 107 C; 119 G; 143 T; 0 other;
SQ
Query Match 20.2%; Score 363.2; DB 23; Length 480;
Best Local Similarity 91.0%; Pred. No. 2.5e-102;
Matches 386; Conservative 0; Mismatches 38; Indels 0; Gaps 0;
QY 117 TTGAAAAGTGATATATAAAGGAACCAAGGAGAAAATTCAGAGGAAGAAAATTC 176
b 57 TTTTACAGGTGTAACCTAAAAGCTAGTTGGTCTTAACCTTGTGTCTTTGTCTTATAAGC 116
QY 177 CTCTGCAGGTGTGCGAGCAGGATTGCTTCTGCAACAAGAGCTCCACCCAGCCACATCTT 236
b 117 CTCTGCAGGTGTGCGAGCAGGATTGCTTCTGCAACAAGAGCTCCACCCAGCCACATCTT 176
QY 237 GGGAAAAGATGGCCACTTCTTGGGGCACAGTCTTTTTCATGTGCTGGTGGTATCCTGTGTT 296
b 177 GGGAAAAGATGGCCACTTCTTGGGGCACAGTCTTTTTCATGTGCTGGTGGTATCCTGTGTT 236
QY 297 TGCAGCGCTGTCTCCACAGGAACCAAGCAGACCTTGGTTGAGGGTATCTTCCGTCTTCC 356
b 237 TGCAGCGCTGTCTCCACAGGAACCAAGCAGACCTTGGTTGAGGGTATCTTCCGTCTTCC 296
QY 357 ATGTGCCCCATCAATGTGCGCCAGCAGCACCTTGTATGGAATTATGTTGATGCGAGGAGC 416
b 297 ATGTGCCCCATCAATGTGCGCCAGCAGCACCTTGTATGGAATTATGTTGATGCGAGGAGC 356
QY 417 ACTGGAACCTCGAATTCATGTTTACACCTTTGTGCAAGAAATGCCAGGACAGCTTCCAAAT 476
b 357 ACTGGAACCTCGAATTCATGTTTACACCTTTGTGCAAGAAATGCCAGGACAGCTTCCAAAT 416
QY 477 CTAGAAGGGGAAGTTTTTGAATCTGTGAAGCCAGGACTTTCTGCTTTTGTAGATCAACCT 536
b 417 CTAGAAGGGGAAGTTTTTGAATCTGTGAAGCCAGGACTTTCTGCTTTTGTAGATCAACCT 476
QY 537 AAGC 540
b 477 AAGC 480
RESULT 15
ABV28387
ID ABV28387 standard; cDNA; 480 BP.
XX
AC ABV28387;
XX
DT 16-SEP-2002 (first entry)
XX Human prostate expression marker cDNA 28378.
DE

X Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
W pharmacogenomic marker; gene; ss.
X Homo sapiens.
X WO2C0160860-A2.
X 23-AUG-2001.
X 20-FEB-2001; 2001WO-US05171.
X 17-FEB-2000; 2000US-183319P.
R 16-MAR-2000; 2000US-189862P.
R 25-MAY-2000; 2000US-207454P.
R 09-JUN-2000; 2000US-211314P.
R 18-JUL-2000; 2000US-219007P.
R 13-DEC-2000; 2000US-255281P.
X (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
X Schlegel R, Endege WO, Monahan JE;
X WPI; 2001-662795/76.
X Novel isolated nucleic acid molecule associated with cancerous state of
T prostate cells and correlating with presence of prostate cancer, useful
T for detecting presence of prostate cancer, stage of prostate cancer -
X Claim 1; Page 5917; 1:750pp; English.
X The invention relates to an isolated nucleic acid molecule (1) comprising
C a nucleotide sequence given in Tables 1-9 (ABV0010-ABV62213) of the
C specification or its complement. (1) is useful for:
C (a) assessing whether a patient is afflicted with prostate cancer;
C (b) monitoring the progression of prostate cancer in a patient;
C (c) assessing the efficacy of a test compound to inhibit prostate
C cancer in a patient;
C (d) assessing the efficacy of a therapy for inhibiting prostate cancer
C in a patient;
C (e) selecting a composition for inhibiting prostate cancer in a patient;
C (f) assessing the prostate cell carcinogenic potential of a compound;
C (g) determining whether prostate cancer has metastasized in a patient;
C (h) assessing the aggressiveness or indolence of prostate cancer in a
C patient;
C (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
X Sequence 480 BP; 1:1 A; 107 C; 119 G; 143 T; 0 other;

Query Match 20.2%; Score 363.2; DB 23; Length 480;
Best Local Similarity 91.0%; Pred. No. 2.5e-102;
Matches 386; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

Y 117 TTGAAAGTGTATATAAAGGAACCAAGGAGAAATTCAGAGGAAGAAAGAAATTC 176
D TTTACAGGTGTAACATAAAAGCTAGTGGTCTAATCTGTGTCTTTGTCTATAAGC 116

Y 177 CTCTGCAGGTGCGAGCAGGATTGCTTCTGCAACAAAGCCTCCACCCAGCCATCTT 236
D TTTACAGGTGCGAGCAGGATTGCTTCTGCAACAAAGCCTCCACCCAGCCATCTT 176

Y 237 GGGAAAGATGGCCACTTCTTGGGCACAGTCTTTTTCATGCTGGTGGTATCCTGTGT 296
D TTTACAGGTGCGAGCAGGATTGCTTCTGCAACAAAGCCTCCACCCAGCCATCTT 236

Y 297 TGCAGCGCTGTCTCCACAGGAACCAAGCAGACTTGGTTTGGGGTATCTTCTGTCTCC 356
D TTTACAGGTGCGAGCAGGATTGCTTCTGCAACAAAGCCTCCACCCAGCCATCTT 296

Y 357 ATGTGCCCCCATCAATGTCAGCGCCAGCACCTTGTATGGATTATGTTTATGTCAGGGAGC 416
D TTTACAGGTGCGAGCAGGATTGCTTCTGCAACAAAGCCTCCACCCAGCCATCTT 356

Qy 417 ACTGGAACTCGAATTCATGTTTACACCTTTGTGCAGAAAATGCCAGGACAGCTTCCAATT 476
Db 357 ACTGGAACTCGAATTCATGTTTACACCTTTGTGCAGAAAATGCCAGGACAGCTTCCAATT 416

Qy 477 CTAGAAGGGGAAGTTTGTATTCTGTGAAGCCAGGACTTTCTGCTTTTGTAGATCAACCT 536
Db 417 CTAGAAGGGGAAGTTTGTATTCTGTGAAGCCAGGACTTTCTGCTTTTGTAGATCAACCT 476

Qy 537 AAGC 540
Db 477 AAGC 480

Search completed: October 6, 2003, 11:14:53
Job time : 381 secs

ORIGIN

Query Match: 87.5%; Score 1575; DB 6: Length 1998;

Best Local Similarity 98.2%; Pred. No. 0;

Base local similarity	98.2%	freq.no:	0;	
Matches 1620;	Conservative	2;	Mismatches	2;
			Indels	25;
			Gaps	2;

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QY	84	TC	CATACAGACAAGATCAT	TATGGTGTCTGTT	-----AGGTTG	119
DB	61	TC	CATACAGACAAGATCAT	TATGGTGTCTGTTAGGTAGGACTTGTATCCAGATGTAAGGTTG	150	
QY	120	AAAA	AGTGATATAATAAAGGAACCAAGGAGAAATTCAGAAGGAAAGAAATAATTCGCTG	179		
DB	121	AAAA	AGTGATATAATAAAGGAACCAAGGAGAAATTCAGAAGGAAAGAAATAATTCGCTG	180		
QY	180	TGC	AGTGTCGAGCAGGATGCTTCTGCAACAAAAGCCTCCACCCAGCCACATCTGGG	239		
DB	181	TGC	AGTGTCGAGCAGGATGCTTCTGCAACAAAAGCCTCCACCCAGCCACATCTGGG	240		
QY	240	AAA	AGNATGGCCACTTCTTTGGGGCACAGTCTTTTTCATGCTGGTGGTATCTGTGTTTGC	299		
DB	241	AAA	AGNATGGCCACTTCTTTGGGGCACAGTCTTTTTCATGCTGGTGGTATCTGTGTTTGC	300		
QY	300	AGC	GTCTCTCCACAGGAACCCAGCAGACTTGGTTTGAGGGTATCTTCTGTCTTCCATG	359		
DB	301	AGC	GTCTCTCCACAGGAACCCAGCAGACTTGGTTTGAGGGTATCTTCTGTCTTCCATG	360		
QY	360	TGCC	CCATCAATGTCAGCGCCAGCACCTTGTATGGAATATGTTTGATGCGAGGACACT	419		
DB	361	TGCC	CCATCAATGTCAGCGCCAGCACCTTGTATGGAATATGTTTGATGCGAGGACACT	420		
QY	420	GGA	ACTCGAATTCATGTTTACACCTTTGTGCAGAAATGCGCAGGACAGCTTCCAAATCTA	479		
DB	421	GGA	ACTCGAATTCATGTTTACACCTTTGTGCAGAAATGCGCAGGACAGCTTCCAAATCTA	480		
QY	480	GAA	GGGAAGTTTTGTATTCGTGAAGCCAGGACTTTCTGCTTTTGTAGATCAACCTAAG	539		
DB	481	GAA	GGGAAGTTTTGTATTCGTGAAGCCAGGACTTTCTGCTTTTGTAGATCAACCTAAG	540		
QY	540	CAG	GTGCTGAGACCGTTCAGGGCTCTTAGAGGTGGCCAAAGACTCAATCCCCCGAAGT	599		
DB	541	CAG	GTGCTGAGACCGTTCAGGGCTCTTAGAGGTGGCCAAAGACTCAATCCCCCGAAGT	600		
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QY	720	GTAC	CAAGGGCCAGTGTTAGCATCATGGATGGATCCGACGAAGGCATATAGCTTGGGTT	779		
DB	721	GTAC	CAAGGGCCAGTGTTAGCATCATGGATGGATCCGACGAAGGCATATAGCTTGGGTT	780		
QY	780	ACT	GTGAATTTTGTACAGGTGAGCTGCATGGCCACAGACAGGAGACTGTGGGACCTTG	839		
DB	781	ACT	GTGAATTTTGTACAGGTGAGCTGCATGGCCACAGACAGGAGACTGTGGGACCTTG	840		
QY	840	GAC	CTAGGGAGCCTCCACCCCAATCACGTTCTCTGCCCCAGTTTGAGAAACTCTGGAA	899		
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QY	959	CAAA	CTCCTAGGGGCTACCTCACTTCTCTTTGAGATGTTTAAACAGCAGCTTATAAGCTCTAT	959		
DB	960	CAAA	CTCCTAGGGGCTACCTCACTTCTCTTTGAGATGTTTAAACAGCAGCTTATAAGCTCTAT	960		
QY	1019	GG	TTTGGATTGAAAGCTGCAGAGCTAGCAACCTTGGGAGCCCTG	1019		
DB	1020	GG	TTTGGATTGAAAGCTGCAGAGCTAGCAACCTTGGGAGCCCTG	1020		

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.
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earched: 569978 seqs, 220691566 residues

otal number of hits satisfying chosen parameters: 1139956

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Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	DB ID	Description
1	1794.8	99.8	1799	4	US-09-608-285A-2
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3	1794.8	99.8	1799	4	US-09-370-265-2
4	1794.8	99.8	1799	4	US-09-557-800C-2
5	1575	87.5	1998	4	US-09-240-639-5
6	1445	80.3	1601	4	US-09-608-285A-24
7	1445	80.3	1601	4	US-09-370-265-24
8	1445	80.3	1601	4	US-09-557-800C-24
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11	1287	71.5	1287	4	US-09-370-265-4
12	1287	71.5	1287	4	US-09-557-800C-4
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16	1277.4	71.0	1287	4	US-09-557-800C-6
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31	303.6	16.9	9365	4	US-09-350-836B-8
32	303.6	16.9	9365	4	US-09-370-265-8
33	303.6	16.9	9365	4	US-09-557-800C-8
34	300	16.7	300	4	US-09-608-285A-1
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ALIGNMENTS

RESULT 1
US-09-608-285A-2
; Sequence 2, Application US/09608285A
; Patent No. 6335013
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 28110/36570
; CURRENT APPLICATION NUMBER: US/09/608,285A
; CURRENT FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/583,231
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 09/557,800
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1799
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (246)..(1529)
; NAME/KEY: misc feature
; LOCATION: (1718)
; OTHER INFORMATION: n = adenine or guanine or cytosine or thymidine
US-09-608-285A-2

Query Match 99.8%; Score 1794.8; DB 4; Length 1799;
Best Local Similarity 100.0%; Pred. NO. 0;
Matches 1799; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1 GCGGGTGC CGCGCAAGGTTGGCGCGCGGTTTCCTTCTGTTCCCTGGTCAACAAAGAAA 60
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; Patent No. 6387645
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 28110/35761
; CURRENT APPLICATION NUMBER: US/09/350,836B
; CURRENT FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1799

TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (246)..(1529)
NAME/KEY: misc_feature
LOCATION: (1718)
OTHER INFORMATION: n = adenine or guanine or cytosine or thymine
S-09-350-836B-2

Query Match 99.8%; Score 1794.8; DB 4; Length 1799;
Best Local Similarity 100.0%; Pred. No. C;
Matches 1799; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GCGGGCTGCGCGCAAGGGTGGCGCGCGCGCTTTCCCTTGTTCCCTGGTCAACAAGAAA 60
b
1 GCGGGCTGCGCGCAAGGGTGGCGCGCGCGCTTTCCCTTGTTCCCTGGTCAACAAGAAA 60
61 TGTGGAGTGTCTTGGCTGAATCCTCATACAGACAAGATCATATTATGGTGTGTAGGTTGA 120
b 61 TGTGGAGTGTCTTGGCTGAATCCTCATACAGACAAGATCATATTATGGTGTGTAGGTTGA 120
121 AAAAGTGATATAATAAAGGAACCAAGGAGAGAAAATTCAGAAAGGAAAGAAAATTCCTCT 180
b 121 AAAAGTGATATAATAAAGGAACCAAGGAGAGAAAATTCAGAAAGGAAAGAAAATTCCTCT 180
181 GCAGGTGTGCGAGCAGGATTGCTTCTGCAACAAAGCCTCCACCCAGCCACATCTTGGGA 240
b 181 GCAGGTGTGCGAGCAGGATTGCTTCTGCAACAAAGCCTCCACCCAGCCACATCTTGGGA 240
241 AAAGAATGGCCACTTCTTGGGCACAGTCTTTTTCATGCTGGTGGTATCCTGRTTGGCA 300
b 241 AAAGAATGGCCACTTCTTGGGCACAGTCTTTTTCATGCTGGTGGTATCCTGRTTGGCA 300
301 GCGTGTCTCCACAGGAACCCAGCAGACTTGGTTTGAGGGTATCTTCCCTGCTCCATGT 360
b 301 GCGTGTCTCCACAGGAACCCAGCAGACTTGGTTTGAGGGTATCTTCCCTGCTCCATGT 360
361 GCCCCATCAATGTCAGCGCCAGCACCTTGTATGGAATTATGTTGATGCAGGGAGCACTG 420
b 361 GCCCCATCAATGTCAGCGCCAGCACCTTGTATGGAATTATGTTGATGCAGGGAGCACTG 420
421 GAACTCGAATTCATGTTTACACCTTTGTGCAGAAAAATGCCAGGACAGCTTCCAATTCTAG 480
b 421 GAACTCGAATTCATGTTTACACCTTTGTGCAGAAAAATGCCAGGACAGCTTCCAATTCTAG 480
481 AAGGGGAAGTTTTTGATTCTGTGAAGCCAGGACTTTCTGCTTTTGTAGATCAACCTAAGC 540
b 481 AAGGGGAAGTTTTTGATTCTGTGAAGCCAGGACTTTCTGCTTTTGTAGATCAACCTAAGC 540
541 AGGTGCTGAGACCGTTCAAGGGCTCTTAGAGGTGGCCAAAGACTCAATCCCGCAAGTC 600
b 541 AGGTGCTGAGACCGTTCAAGGGCTCTTAGAGGTGGCCAAAGACTCAATCCCGCAAGTC 600
601 ACTGGAATAAGACCCCAAGTGGTCTAAAGGCAACAGCAGGACTACGCTTACTGCCAGAAC 660
b 601 ACTGGAATAAGACCCCAAGTGGTCTAAAGGCAACAGCAGGACTACGCTTACTGCCAGAAC 660
661 ACAAGGCCAAGGCTCTGCTCTTTGAGGTAAAGGAGATCTTCAGGAAGTCAACCTTCCTGG 720
b 661 ACAAGGCCAAGGCTCTGCTCTTTGAGGTAAAGGAGATCTTCAGGAAGTCAACCTTCCTGG 720
721 TACCAAGGGCAGTGTTAGCATCATGGATGGATCCGACGAGGCAATATTAGCTTGGGTTA 780
b 721 TACCAAGGGCAGTGTTAGCATCATGGATGGATCCGACGAGGCAATATTAGCTTGGGTTA 780
781 CTGTGAATTTCTGACAGGTCACTGCATGGCCACAGACAGGAGACTGTGGGGACCTTGG 840
b 781 CTGTGAATTTCTGACAGGTCACTGCATGGCCACAGACAGGAGACTGTGGGGACCTTGG 840
841 ACCTAGGGGAGCCTCCACCCCAATCACGTTCCCTGCCCCAGTTTGGAGAAACTCTGGAAC 900
b 841 ACCTAGGGGAGCCTCCACCCCAATCACGTTCCCTGCCCCAGTTTGGAGAAACTCTGGAAC 900

901 AAACCTCCTAGGGCTACCTCACCTTCCCTTTGAGATGTTTAAACAGCACCTTATTAAGCTCTATA 960
Db
901 AAACCTCCTAGGGCTACCTCACCTTCCCTTTGAGATGTTTAAACAGCACCTTATTAAGCTCTATA 960
961 CACATAGTTACCTGGGATTGGATTGAAAGCTGCAAGACTAGCAACCTTGGGAGCCCTGG 1020
Db
961 CACATAGTTACCTGGGATTGGATTGAAAGCTGCAAGACTAGCAACCTTGGGAGCCCTGG 1020
1021 AGACAGAAGGGACTGATGGGCACACTTTCGGGAGTGCCTGTTTACCGAGATGGTTGGAAG 1080
Db
1021 AGACAGAAGGGACTGATGGGCACACTTTCGGGAGTGCCTGTTTACCGAGATGGTTGGAAG 1080
1081 CAGAGTGGATCTTTGGGGTGTGAAATACCACTATCCAGTATGCTGTCCTTACTATTATGACCGAGCTTGACA 1140
Db
1081 CAGAGTGGATCTTTGGGGTGTGAAATACCACTATCCAGTATGCTGTCCTTACTATTATGACCGAGCTTGACA 1140
1141 GCTTTGAGCCCTGCTATGCGGAAGTCTGAGGGTGGTACGAGGAAAACTTACACAGCCAG 1200
Db
1141 GCTTTGAGCCCTGCTATGCGGAAGTCTGAGGGTGGTACGAGGAAAACTTACACAGCCAG 1200
1201 AGGAGTCCAGAGAGGTTCCCTTCTATGCTTCTTACTATTATGACCGAGCTTGACA 1260
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1201 AGGAGTCCAGAGAGGTTCCCTTCTATGCTTCTTACTATTATGACCGAGCTTGACA 1260
1261 CAGACATGATTGATTATGAAAGGGGGGTATTTTAAAGTTGAAGATTTTGAAGAAAAAG 1320
Db
1261 CAGACATGATTGATTATGAAAGGGGGGTATTTTAAAGTTGAAGATTTTGAAGAAAAAG 1320
1321 CCAGGGAAGTGTGTGATTAACCTTGGAAAACTTCCACCTCAGGCAGTCCCTTTCCCTGTCATGG 1380
Db
1321 CCAGGGAAGTGTGTGATTAACCTTGGAAAACTTCCACCTCAGGCAGTCCCTTTCCCTGTCATGG 1380
1381 ATCTCAGCTACATCACAGCCCTGTTAAAGGATGGCTTTGGCTTTGCAGACAGCACAGTCT 1440
Db
1381 ATCTCAGCTACATCACAGCCCTGTTAAAGGATGGCTTTGGCTTTGCAGACAGCACAGTCT 1440
1441 TACAGCTCAGAAAAAGTGAACAAACATAGAGACGGGCTGGGCTTGGGGCCACCTTTC 1500
Db
1441 TACAGCTCAGAAAAAGTGAACAAACATAGAGACGGGCTGGGCTTGGGGCCACCTTTC 1500
1501 ACCTGTTGCAGTCTCTGGSCATCTCCCATTTGAGGCCACGTACTTCCCTTGGAGACCTGCAT 1560
Db
1501 ACCTGTTGCAGTCTCTGGSCATCTCCCATTTGAGGCCACGTACTTCCCTTGGAGACCTGCAT 1560
1561 TTGCCAACACACCTTTTAAAGGGAGGAGAGACACTTAGTCTCTGAACCTAGTCTGGGACA 1620
Db
1561 TTGCCAACACACCTTTTAAAGGGAGGAGAGACACTTAGTCTCTGAACCTAGTCTGGGACA 1620
1621 TCCTGGACTTGAGCCTAGAGATTWRGTTAATTAASCGGCGAGCTTATCCTTTWATRAGGT 1680
Db
1621 TCCTGGACTTGAGCCTAGAGATTWRGTTAATTAASCGGCGAGCTTATCCTTTWATRAGGT 1680
1681 AATTACTTGCTGCTGGCGGCTTTACACGTCTGATGAGGAAAACTTCCGTCCTCAACTAACGC 1740
Db
1681 AATTACTTGCTGCTGGCGGCTTTACACGTCTGATGAGGAAAACTTCCGTCCTCAACTAACGC 1740
1741 TTGASAMATCCCTTCCGAGCTGCGATACACGCTGATGAGGAAAACTTCCGTCCTCAACTAACGC 1799
Db
1741 TTGASAMATCCCTTCCGAGCTGCGATACACGCTGATGAGGAAAACTTCCGTCCTCAACTAACGC 1799

RESULT 3
US-09-370-265-2
; Sequence 2, Application US/09370265
; Patent No. 6447771
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
; FILE REFERENCE: 28111/35908
; CURRENT APPLICATION NUMBER: US/09/370,265

CURRENT FILING DATE: 1999-08-09
EARLIER APPLICATION NUMBER: PCT/US99/16180
EARLIER FILING DATE: 1999-07-16
EARLIER APPLICATION NUMBER: 09/350,836
EARLIER FILING DATE: 1999-07-09
EARLIER APPLICATION NUMBER: 09/273,447
EARLIER FILING DATE: 1999-03-19
EARLIER APPLICATION NUMBER: 09/244,444
EARLIER FILING DATE: 1999-02-04
EARLIER APPLICATION NUMBER: 09/122,449
EARLIER FILING DATE: 1998-07-24
EARLIER APPLICATION NUMBER: 09/118,205
EARLIER FILING DATE: 1998-07-16
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 2
LENGTH: 1799
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (246)..(1529)
FEATURE:
NAME/KEY: misc feature
LOCATION: (1718)
OTHER INFORMATION: n = adenine or guanine or cytosine or thymine

S-09-370-265-2

Query Match: 99.8%; Score 1794.8; DB 4; Length 1799;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1799; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

y	1	GC	GGGTGCGCGCAAGGGTGGCGCGCGCGCTTTCCCTGTTCCCTGGTCAACAAAGAAA	60
b	1	GC	GGGTGCGCGCAAGGGTGGCGCGCGCGCTTTCCCTGTTCCCTGGTCAACAAAGAAA	60
y	61	TG	TGAGAGTGTCTTGGCTGAATCCTCATACAGACAAGATCATTTATGGTGTAGGTTGA	120
b	61	TG	TGAGAGTGTCTTGGCTGAATCCTCATACAGACAAGATCATTTATGGTGTAGGTTGA	120
y	121	AA	AAAGTGATATAATAAAGGAACCAAGGAGAGAAATTCAGAGGAAGAAATAATGCCCTCT	180
b	121	AA	AAAGTGATATAATAAAGGAACCAAGGAGAGAAATTCAGAGGAAGAAATAATGCCCTCT	180
y	181	GC	AGGTGTCGGAGCAGGATTGCTTCTGCAACAAAGCCCTCCACCCAGCCACATCTGGGA	240
b	181	GC	AGGTGTCGGAGCAGGATTGCTTCTGCAACAAAGCCCTCCACCCAGCCACATCTGGGA	240
y	241	AA	AGAAATGGCCACTTCTTTGGGGCACAGTCTTTTTCATGCTGGTGGTATCCTGTGTTGCA	300
b	241	AA	AGAAATGGCCACTTCTTTGGGGCACAGTCTTTTTCATGCTGGTGGTATCCTGTGTTGCA	300
y	301	GC	GCTGTCTCCACAGGAACCCAGCAGACTTGGTTTGAGGGTATCTTCTCTCTCCATGT	360
b	301	GC	GCTGTCTCCACAGGAACCCAGCAGACTTGGTTTGAGGGTATCTTCTCTCTCCATGT	360
y	361	GC	CCATCAATGTACAGCCAGCACCTTGTATGGAAATTATGTTGATGCAGGGAGCACTG	420
b	361	GC	CCATCAATGTACAGCCAGCACCTTGTATGGAAATTATGTTGATGCAGGGAGCACTG	420
y	421	GA	ACTCGAATTTCATGTTTACACCTTTGTGCAGAAATGCCAGGACAGCTTCCAAATCTAG	480
b	421	GA	ACTCGAATTTCATGTTTACACCTTTGTGCAGAAATGCCAGGACAGCTTCCAAATCTAG	480
y	481	AA	GGGGAAGTTTCTGATCTGTGAAGCCAGGACTTTCTGCTTTTGTAGATCAACCTAAGC	540
b	481	AA	GGGGAAGTTTCTGATCTGTGAAGCCAGGACTTTCTGCTTTTGTAGATCAACCTAAGC	540
y	541	AG	GGTGTGAGACCGTTCAAGGGCTCTTAGAGGTGGCCCAAGACTCAATCCCCCGAAGTC	600
b	541	AG	GGTGTGAGACCGTTCAAGGGCTCTTAGAGGTGGCCCAAGACTCAATCCCCCGAAGTC	600
y	601	AC	TGGAAAGAGCCCCAGTGGTCTCTAAAGGCAACAGCAGGACTACGCTTACTGCCAGAAC	660

Db	601	ACTG	AAAAAGACCC	CAGTGTCTCTAAAGGCAACAGCAGGACTACGCTTACTGCCAGAAC	660
Qy	661	ACAA	AGCCAAAGGCTCTGCTCTTTGAGGTAAGGAGATCTTCAGGAAGTCACCTTTCTCTGG	720	
Db	661	ACAA	AGCCAAAGGCTCTGCTCTTTGAGGTAAGGAGATCTTCAGGAAGTCACCTTTCTCTGG	720	
Qy	721	TACC	AAAGGGCAGTGTTAGCATCATGGATCGGATCCGACGAAGGCATATTAGCTTGGTTA	780	
Db	721	TACC	AAAGGGCAGTGTTAGCATCATGGATCGGATCCGACGAAGGCATATTAGCTTGGTTA	780	
Qy	781	CTGT	GAATTTTCTGACAGGTGAGTGCATGGCCACAGACAGGAGACTGTGGGGACCTTGG	840	
Db	781	CTGT	GAATTTTCTGACAGGTGAGTGCATGGCCACAGACAGGAGACTGTGGGGACCTTGG	840	
Qy	841	ACCT	AGGGGGAGCCTCCACCCAAATCACGTTCCCTGCCCCAGTTTGAGAAACTCTGGAAC	900	
Db	841	ACCT	AGGGGGAGCCTCCACCCAAATCACGTTCCCTGCCCCAGTTTGAGAAACTCTGGAAC	900	
Qy	901	AACT	CTCTAGGGGTACCTCACCTTCCCTTTGAGATGTTTAAACAGCACTTATAAGCTCTATA	960	
Db	901	AACT	CTCTAGGGGTACCTCACCTTCCCTTTGAGATGTTTAAACAGCACTTATAAGCTCTATA	960	
Qy	961	CACA	TAGTTACCTGGGATTGGATTGAAAGCTGCAAGACTAGCAACCCCTGGGAGCCTGG	1020	
Db	961	CACA	TAGTTACCTGGGATTGGATTGAAAGCTGCAAGACTAGCAACCCCTGGGAGCCTGG	1020	
Qy	1021	AGAC	AGAAGGACTGATGSGGCACACTTTCCCGAGTGCCTGTTTACCAGATGTTTGAAG	1080	
Db	1021	AGAC	AGAAGGACTGATGSGGCACACTTTCCCGAGTGCCTGTTTACCAGATGTTTGAAG	1080	
Qy	1081	CAGAG	TGGATCTTTGGGGGTGTGAAATACCAGTATGTGGCAACCAAGAGGGGAGGTGG	1140	
Db	1081	CAGAG	TGGATCTTTGGGGGTGTGAAATACCAGTATGTGGCAACCAAGAGGGGAGGTGG	1140	
Qy	1141	GCTT	TGAGCCCTGCTATGCCGAAGTGTGAGGGTGTACGAGGAACCTTCACCAAGCAG	1200	
Db	1141	GCTT	TGAGCCCTGCTATGCCGAAGTGTGAGGGTGTACGAGGAACCTTCACCAAGCAG	1200	
Qy	1201	AGGAG	TCCAGAGAGGTTCCTTCTATGCTTTCTCTTACTATTATGACCGAGCTGTTGACA	1260	
Db	1201	AGGAG	TCCAGAGAGGTTCCTTCTATGCTTTCTCTTACTATTATGACCGAGCTGTTGACA	1260	
Qy	1261	CAGAC	ATGATTGATTATGAAAGGGGGTACTTTTAAAGTTGAAGATTTTGAAGAAAAAG	1320	
Db	1261	CAGAC	ATGATTGATTATGAAAGGGGGTACTTTTAAAGTTGAAGATTTTGAAGAAAAAG	1320	
Qy	1321	CCAG	GGAAGTGTGTATTAACCTTGGAAAACTTCACCTCAGGAGTCCCTTCTGTGCAATG	1380	
Db	1321	CCAG	GGAAGTGTGTATTAACCTTGGAAAACTTCACCTCAGGAGTCCCTTCTGTGCAATG	1380	
Qy	1381	ATCT	CAGCTACATCACAGCCCTGTTAAAGGATGGCTTTGGCTTTCAGACAGCACAGTCT	1440	
Db	1381	ATCT	CAGCTACATCACAGCCCTGTTAAAGGATGGCTTTGGCTTTCAGACAGCACAGTCT	1440	
Qy	1441	TACAG	CTCACAAGAAAGTGAACACATAGAGACGGGCTGGGCCCTTGGGGCCACCTTTC	1500	
Db	1441	TACAG	CTCACAAGAAAGTGAACACATAGAGACGGGCTGGGCCCTTGGGGCCACCTTTC	1500	
Qy	1501	ACCT	GTTGCAGTCTCTGGGCATCTCCCATTTGAGGCCACGTACTTCTCTGGAGACCTGCAT	1560	
Db	1501	ACCT	GTTGCAGTCTCTGGGCATCTCCCATTTGAGGCCACGTACTTCTCTGGAGACCTGCAT	1560	
Qy	1561	TTGC	CAACACCTTTTAAAGGGAGGAGAGACACTTAGTTTCTGAACCTAGTCTGGGGACA	1620	
Db	1561	TTGC	CAACACCTTTTAAAGGGAGGAGAGAGACACTTAGTTTCTGAACCTAGTCTGGGGACA	1620	
Qy	1621	TCCT	TGACTTGAGCCTAGAGATTWRGTTAATTAASCGGCGAGCTTATCCTTWTATAGGT	1680	
Db	1621	TCCT	TGACTTGAGCCTAGAGATTWRGTTAATTAASCGGCGAGCTTATCCTTWTATAGGT	1680	
Qy	1681	AA	TTTACTTGCTGGCCCGCTTACACGTGCTGATGGAACCTCGTCCCAACTAACGC	1740	
Db	1681	AA	TTTACTTGCTGGCCCGCTTACACGTGCTGATGGAACCTCGTCCCAACTAACGC	1740	

1681 AATTACTTGCMTGGCCGGCTTTACACGTCGTGATCGNAAACCTCGTCCCAACTAACGC 1740
1741 TTGASAMATCCCCCTTCGCAGCTCGGATACCAAAAGCCGACGACGCTTCCACAGTGCCA 1799
1741 TTGASAMATCCCCCTTCGCAGCTCGGATACCAAAAGCCGACGACGCTTCCACAGTGCCA 1799

RESULT 4
-09-557-800C-2
Sequence 2, Application US/09557800C
Patent No. 6476211
GENERAL INFORMATION:
APPLICANT: Ford, John
APPLICANT: Mulero, Julio
APPLICANT: Yeung, George
TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 28110/36457

CURRENT APPLICATION NUMBER: US/09/557,800C
CURRENT FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/481,238
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: 09/370,265
PRIOR FILING DATE: 1999-08-09
PRIOR APPLICATION NUMBER: PCT/US99/16180
PRIOR FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: 09/350836
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 09/273447
PRIOR FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: 09/122449
PRIOR FILING DATE: 1998-07-24
PRIOR APPLICATION NUMBER: 09/244444
PRIOR FILING DATE: 1999-02-04
PRIOR APPLICATION NUMBER: 09/118,205
PRIOR FILING DATE: 1998-07-16
NUMBER OF SEQ ID NOS: 56
SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 2
LENGTH: 1799
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (246)..(1529)
FEATURE:
NAME/KEY: misc feature
LOCATION: (1718)
OTHER INFORMATION: n = adenine or guanine or cytosine or thymidine
S-09-557-800C-2

Query Match 99.8%; Score 1794.8; DB 4; Length 1799;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1799; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 GCGGGCTGCGCGCAAGGGTGGCGCGCGCGTTCCTTGTTCCCTGGTCAACAAGAA 60
b 1 GCGGGCTGCGCGCAAGGGTGGCGCGCGCGTTCCTTGTTCCCTGGTCAACAAGAA 60
Y 61 TGTGGACTGCTTGGCTGAATCCTCATAACAGACAAGATCATTATGGTCTGTAGGTGA 120
b 61 TGTGGAGTGTCTTGGCTGAATCCTCATAACAGACAAGATCATTATGGTCTGTAGGTGA 120
Y 121 AAAAGTCAATATAAAGGAACCAAGGAGAAAAATTCAGAGGAAAGAAAAATTCGCTCT 180
b 121 AAAAGTCAATATAAAGGAACCAAGGAGAAAAATTCAGAGGAAAGAAAAATTCGCTCT 180
Y 181 GCAGGTGCGGAGCAGGATTGCTTCTGCAACAAAAGCCTCCACCCAGCCACATCTTGGGA 240
b 181 GCAGGTGCGGAGCAGGATTGCTTCTGCAACAAAAGCCTCCACCCAGCCACATCTTGGGA 240
Y 241 AAAGATGGCCACCTCTTGGGACACAGTCTTTTTCATGCTGGTGGTATCCTGTGTTGCA 300
b 241 AAAGATGGCCACCTCTTGGGACACAGTCTTTTTCATGCTGGTGGTATCCTGTGTTGCA 300

Db 241 AAAGAATGGCCACTTCTTGGGGCACAGTCTTTTTCATGCTGGTGGTATCCTGTGTTGCA 300
Qy 301 GCGCTGTCTCCCACAGGAACACAGACACTTGGTTTGAGGGTATCTTCTGTCTTCCATGT 360
Db 301 GCGCTGTCTCCCACAGGAACACAGACACTTGGTTTGAGGGTATCTTCTGTCTTCCATGT 360
Qy 361 GCGCCATCAATGTGAGCCAGCACCTTGTATGGAATATGTTGATGAGGGAGCACTG 420
Db 361 GCGCCATCAATGTGAGCCAGCACCTTGTATGGAATATGTTGATGAGGGAGCACTG 420
Qy 421 GAACTCGAATTCATGTTACACCTTTGTGCAGAAAAATGCCAGGACAGCTTCCCAATTTCTAG 480
Db 421 GAACTCGAATTCATGTTACACCTTTGTGCAGAAAAATGCCAGGACAGCTTCCCAATTTCTAG 480
Qy 481 AAGGGGAAGTTTTTGTATCTGTGAAGCCAGGACTTCTGCTTTTGTAGATCAACCTAAGC 540
Db 481 AAGGGGAAGTTTTTGTATCTGTGAAGCCAGGACTTCTGCTTTTGTAGATCAACCTAAGC 540
Qy 541 AGGCTGCTGAGACCCGTTCAAGGGCTCTTAGAGGTGGCCAAAGACTCAATCCCCCGAAGTC 600
Db 541 AGGCTGCTGAGACCCGTTCAAGGGCTCTTAGAGGTGGCCAAAGACTCAATCCCCCGAAGTC 600
Qy 601 ACTGGAAAAAGACCCCGAGTGGTCTTAAAGGCAACAGCAGGACTACGCTTACTGCCAGAAC 660
Db 601 ACTGGAAAAAGACCCCGAGTGGTCTTAAAGGCAACAGCAGGACTACGCTTACTGCCAGAAC 660
Qy 661 ACAAAGCCAAAGGCTCTGCTCTTTGAGGTAAAGAGATCTTCAGGAAGTCACTTTCTCTGG 720
Db 661 ACAAAGCCAAAGGCTCTGCTCTTTGAGGTAAAGAGATCTTCAGGAAGTCACTTTCTCTGG 720
Qy 721 TACCAAAAGGCGAGTGTAGCATCATGGATCCGACGAAAGGCATATTAGCTTGGGTTA 780
Db 721 TACCAAAAGGCGAGTGTAGCATCATGGATCCGACGAAAGGCATATTAGCTTGGGTTA 780
Qy 781 CTGTGAATTTCTGACAGGTGAGTGCATGGCATGGCGACACAGAGAGACTGTGGGACCTTGG 840
Db 781 CTGTGAATTTCTGACAGGTGAGTGCATGGCATGGCGACACAGAGAGACTGTGGGACCTTGG 840
Qy 841 ACCTAGGGGGAGCCTCCACCCAAATCACGTTCCCTGCCCCAGTTTGAAGAAACTCTGGAAC 900
Db 841 ACCTAGGGGGAGCCTCCACCCAAATCACGTTCCCTGCCCCAGTTTGAAGAAACTCTGGAAC 900
Qy 901 AACTCCTAGGGCTACCTCACTTCCCTTTGAGATGTTTAAACAGCACTTATAAGCTCTATA 960
Db 901 AACTCCTAGGGCTACCTCACTTCCCTTTGAGATGTTTAAACAGCACTTATAAGCTCTATA 960
Qy 961 CACATAGTTACCTGGGATTTGGATTGAAAGCTGCAAGACTAGCAACCTGGGAGCCCTGG 1020
Db 961 CACATAGTTACCTGGGATTTGGATTGAAAGCTGCAAGACTAGCAACCTGGGAGCCCTGG 1020
Qy 1021 AGACAGAAGGGACTGATGGGCACACTTTCCGAGTGCCTGTTTACCGAGATGTTGGAAG 1080
Db 1021 AGACAGAAGGGACTGATGGGCACACTTTCCGAGTGCCTGTTTACCGAGATGTTGGAAG 1080
Qy 1081 CAGAGTGGATCTTTGGGGTGTGAAATACCAAGTATGGTGGCAACCAAGAGGGGAGGTGG 1140
Db 1081 CAGAGTGGATCTTTGGGGTGTGAAATACCAAGTATGGTGGCAACCAAGAGGGGAGGTGG 1140
Qy 1141 GCTTTGAGCCCTGCTATGCCGAAGTCTGAGGGTGGTACGAGGAAAACTTACAGCCAG 1200
Db 1141 GCTTTGAGCCCTGCTATGCCGAAGTCTGAGGGTGGTACGAGGAAAACTTACAGCCAG 1200
Qy 1201 AGGAGTCCAGAGAGGTTCCTTCTATGCTTTCTTACTATTATGACCGAGCTGTTGACA 1260
Db 1201 AGGAGTCCAGAGAGGTTCCTTCTATGCTTTCTTACTATTATGACCGAGCTGTTGACA 1260
Qy 1261 CAGACATGATTGATTGAAAAAGGGGGTATTTTAAAGTTGAAGATTTTGAAGAAAAAG 1320
Db 1261 CAGACATGATTGATTGAAAAAGGGGGTATTTTAAAGTTGAAGATTTTGAAGAAAAAG 1320
Qy 1321 CCAGGGAAGTGTGTGATAAATTGGAAAACTTACCTCAGGCAGTCTTCTGTGTCATGG 1380
Db 1321 CCAGGGAAGTGTGTGATAAATTGGAAAACTTACCTCAGGCAGTCTTCTGTGTCATGG 1380

|||||
1321 GCCAGGGAAGTGTGTGATAACTTGGAAAACTTACCTCAGGCAGTCCCTTTCCTGTGCATG 1380
1380 GATCTCAGCTACATCACAGCCCTGTTAAAGGATGGCTTTGGCTTTGCAGACAGCACAGTC 1439
1381 GATCTCAGCTACATCACAGCCCTGTTAAAGGATGGCTTTGGCTTTGCAGACAGCACAGTC 1440
1440 TTACAGCTCACAAAGAAAGTGAACAACATAGAGACGGGCTGGCCCTTGGGGCCACCTTT 1499
1441 TTACAGCTCACAAAGAAAGTGAACAACATAGAGACGGGCTGGCCCTTGGGGCCACCTTT 1500
1500 CACCTGTTGCAGTCTCTGGGCATCTCCCATTTAGGCCACGTAATCTTCTGGAGACCTGCA 1559
1501 CACCTGTTGCAGTCTCTGGGCATCTCCCATTTAGGCCACGTAATCTTCTGGAGACCTGCA 1560
1560 TTTGCCAACACCTTTTAAAGGGAGGAGAGACGACCTTAGTTTCTGAACTAGTCTGGGGAC 1619
1561 TTTGCCAACACCTTTTAAAGGGAGGAGAGACGACCTTAGTTTCTGAACTAGTCT-GGGAC 1619
1620 ATCCTGGACTTGAGCCTAGAGATTWRGTT 1648
1620 ATCCTGGACTTGAGCCTAGAGATTTAGGT 1648

RESULT 6
S-09-608-285A-24
Sequence 24, Application US/09608285A
Patent No. 6335013
GENERAL INFORMATION:
APPLICANT: Ford, John
APPLICANT: Mulero, Giulio
APPLICANT: Yeung, George
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
TITLE OF INVENTION: POLYPEPTIDES
FILE REFERENCE: 28116/36570
CURRENT APPLICATION NUMBER: US/09/608,285A
CURRENT FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 09/583,231
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 09/557,800
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/481,238
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: 09/370,265
PRIOR FILING DATE: 1999-08-09
PRIOR APPLICATION NUMBER: PCT/US99/16180
PRIOR FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: 09/350,836
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 09/273,447
PRIOR FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: 09/244,444
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PRIOR FILING DATE: 1998-07-24
PRIOR APPLICATION NUMBER: 09/118,205
PRIOR FILING DATE: 1998-07-16
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn ver. 2.0
SEQ ID NO 24
LENGTH: 1601
TYPE: DNA
ORGANISM: Homo sapiens
S-09-608-285A-24

Query Match 80.3%; Score 1445; DB 4: Length 1601;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 GCGGGCTGCCGCGCAAGGGTGGCGCGCGGCTTTCCTTGTTCCTGGTCAACAAAGAAA 60
1 GCGGGCTGCCGCGCAAGGGTGGCGCGCGGCTTTCCTTGTTCCTGGTCAACAAAGAAA 60

QY 61 TGTGGAGTGTCTTGGCTGAATCCTCATACAGACAAGATCATTATGGTGTCTGTAGTTGA 120
DB 61 TGTGGAGTGTCTTGGCTGAATCCTCATACAGACAAGATCATTATGGTGTCTGTAGTTGA 120
QY 121 AAAAGTGATATAATAAAGGAACCAAGAGGAGAAATTCAGAAGGAAAGAAAAAATTCCTCT 180
DB 121 AAAAGTGATATAATAAAGGAACCAAGAGGAGAAATTCAGAAGGAAAGAAAAAATTCCTCT 180
QY 181 GCAGGTGTGCGAGCAGGATTGCTTCTGCAACAAAAAGCCCTCCACCCAGCCACATCTTGGGA 240
DB 181 GCAGGTGTGCGAGCAGGATTGCTTCTGCAACAAAAAGCCCTCCACCCAGCCACATCTTGGGA 240
QY 241 AAAGAATGGCCACTTCTTGGGGCACAGTCTTTTTCATGCTGGTATCCTGTCTTTCGCA 300
DB 241 AAAGAATGGCCACTTCTTGGGGCACAGTCTTTTTCATGCTGGTATCCTGTCTTTCGCA 300
QY 301 GCGCTGTCTCCACAGAACCCAGCAGACTTGGTTGAGGGTATCTTCCCTGTCTTCCATGT 360
DB 301 GCGCTGTCTCCACAGAACCCAGCAGACTTGGTTGAGGGTATCTTCCCTGTCTTCCATGT 360
QY 361 GCGCTGTCTCCACAGAACCCAGCAGACTTGGTTGAGGGTATCTTCCCTGTCTTCCATGT 420
DB 361 GCGCTGTCTCCACAGAACCCAGCAGACTTGGTTGAGGGTATCTTCCCTGTCTTCCATGT 420
QY 421 GAACTCGAATTCATGTTTACACCTTTGTGCGAGAAAAATGCCAGGACAGCTTCCCAATCTAG 480
DB 421 GAACTCGAATTCATGTTTACACCTTTGTGCGAGAAAAATGCCAGGACAGCTTCCCAATCTAG 480
QY 481 AAGGGGAAGTTTTTGTGTTGTGAAGCCAGGACTTCTGCTTTTGTAGATCAACCTAAGC 540
DB 481 AAGGGGAAGTTTTTGTGTTGTGAAGCCAGGACTTCTGCTTTTGTAGATCAACCTAAGC 540
QY 541 AAGGGGAAGTTTTTGTGTTGTGAAGCCAGGACTTCTGCTTTTGTAGATCAACCTAAGC 600
DB 541 AAGGGGAAGTTTTTGTGTTGTGAAGCCAGGACTTCTGCTTTTGTAGATCAACCTAAGC 600
QY 601 ACTGGAAGAACCCAGTGTCTTAAAGGCAACAGCAGGACTACGCTTACTGCCAGAAC 660
DB 601 ACTGGAAGAACCCAGTGTCTTAAAGGCAACAGCAGGACTACGCTTACTGCCAGAAC 660
QY 661 ACAAGCCAAAGGCTCTGCTTTGAGGTAAAGGAGATCTTTCAGGAAGTCCCTTCTCTGG 720
DB 661 ACAAGCCAAAGGCTCTGCTTTGAGGTAAAGGAGATCTTTCAGGAAGTCCCTTCTCTGG 720
QY 721 TACCAAGGGCAGTGTAGCATCATGGATGGATCCGACGAAGGCATATTAGCTTGGTTA 780
DB 721 TACCAAGGGCAGTGTAGCATCATGGATGGATCCGACGAAGGCATATTAGCTTGGTTA 780
QY 781 CTGTGAATTTTCTGACAGTGTGATGCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTG 840
DB 781 CTGTGAATTTTCTGACAGTGTGATGCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTG 840
QY 841 ACCTAGGGGGAGCCTCCACCCAAATCACGTTCTGCTGCTGCTTCTGCTGCTTCTGCTG 900
DB 841 ACCTAGGGGGAGCCTCCACCCAAATCACGTTCTGCTGCTGCTTCTGCTGCTTCTGCTG 900
QY 901 AAACCTCTAGGGGCTACCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 960
DB 901 AAACCTCTAGGGGCTACCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 960
QY 961 CACATAGTTACCTGGGATTTGGATTGAAAGCTGCAAGACTAGCAACCTTGGGAGCCCTGG 1020
DB 961 CACATAGTTACCTGGGATTTGGATTGAAAGCTGCAAGACTAGCAACCTTGGGAGCCCTGG 1020
QY 1021 AGACAGAAGGGACTGATGGGCACACTTTTCCGGAGTGGCTGTTTACCGAGATGGTTGGAAG 1080
DB 1021 AGACAGAAGGGACTGATGGGCACACTTTTCCGGAGTGGCTGTTTACCGAGATGGTTGGAAG 1080
QY 1081 CAGAGTGGATCTTTGGGGGTGTGAATACCAGTATGCTGGCAACCAAGAGGGGAGGTGG 1140
DB 1081 CAGAGTGGATCTTTGGGGGTGTGAATACCAGTATGCTGGCAACCAAGAGGGGAGGTGG 1140
QY 1141 GCTTTGAGCCCTGCTATGCCGAAGTGTCTGAGGGTGTACGAGGAAAAACTTCACCCAGCCAG 1200

b 1141 GCTTGGCCCTGCTATGCCGAAGTCTGAGGGTGGTACGAGGAACCTTCCAGCCAG 1200
y 1201 AGGAGGTCCAGAGAGGTTCCTTCTATGGCTTCTCTACTATTATGACCGAGCTGTGACA 1260
b 1201 AGGAGGTCCAGAGAGGTTCCTTCTATGGCTTCTCTACTATTATGACCGAGCTGTGACA 1260
y 1261 CAGACATGATTGATTATGAAGAGGGGGGATTTTAAAGTTGAAGATTTTGAAGAAAG 1320
b 1261 CAGACATGATTGATTATGAAGAGGGGGGATTTTAAAGTTGAAGATTTTGAAGAAAG 1320
y 1321 CCAGGGAAGTGTGTGATAACTTGGAAAACTTCACCTCAGGCAGTCCCTTCCCTGTGCATGG 1380
b 1321 CCAGGGAAGTGTGTGATAACTTGGAAAACTTCACCTCAGGCAGTCCCTTCCCTGTGCATGG 1380
y 1381 ATCTCAGCTACATCAGCCCTGTTAAAGGATGGCTTTGGCTTTGCAGACAGCACAGTCT 1440
b 1381 ATCTCAGCTACATCAGCCCTGTTAAAGGATGGCTTTGGCTTTGCAGACAGCACAGTCT 1440
y 1441 TACAG 1445
b 1441 TACAG 1445

RESULT 7
S-09-370-265-24
Sequence 24, Application US/09370265
Patent No. 6447771
GENERAL INFORMATION:
APPLICANT: Ford, John
APPLICANT: Mulero, Julio
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
TITLE OF INVENTION: POLYPEPTIDES
FILE REFERENCE: 28111/35908
CURRENT APPLICATION NUMBER: US/09/370,265
CURRENT FILING DATE: 1999-08-09
EARLIER APPLICATION NUMBER: PCT/US99/16180
EARLIER FILING DATE: 1999-07-16
EARLIER APPLICATION NUMBER: 09/350,836
EARLIER FILING DATE: 1999-07-09
EARLIER APPLICATION NUMBER: 09/273,447
EARLIER FILING DATE: 1999-03-19
EARLIER APPLICATION NUMBER: 09/244,444
EARLIER FILING DATE: 1999-02-04
EARLIER APPLICATION NUMBER: 09/122,449
EARLIER FILING DATE: 1998-07-24
EARLIER APPLICATION NUMBER: 09/118,205
EARLIER FILING DATE: 1998-07-16
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 24
LENGTH: 1601
TYPE: DNA
ORGANISM: Homo sapiens
S-09-370-265-24

Query Match 80.3%; Score 1445; DB 4; Length 1601;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GCGGGCTGCGCGCAAGGGTGGCGCGCGGCTTTCCTTGTTCCTGGTCAACAAAGAA 60
1 GCGGGCTGCGCGCAAGGGTGGCGCGCGGCTTTCCTTGTTCCTGGTCAACAAAGAA 60

61 TGTGGAGTCTCTGGCTGAATCCCTCATACAGACAAGATCATTATGGTGTAGTTGA 120
61 TGTGGAGTCTCTGGCTGAATCCCTCATACAGACAAGATCATTATGGTGTAGTTGA 120

121 AAAAGTATATAATAAGGAACCAAGGAGAAAAATTCAGAAGGAAGAAAAAATTGCCCTCT 180
121 AAAAGTATATAATAAGGAACCAAGGAGAAAAATTCAGAAGGAAGAAAAAATTGCCCTCT 180

181 GCAGGTGTGGAGCAGGATTGCTTCTGTGCAACAAAGGCTCCACCCAGCCACATCTTTGGGA 240

Db 181 GCAGGTGTGGAGCAGGATTGCTTCTGTCAACAAAGCCTCCACCCAGCCACATCTTGGGA 240
Qy 241 AAAGAATGGCCACTTCTTGGGGCACAGTCTTTTTCATGCTGGTGGTATCCTGTGTTGCA 300
Db 241 AAAGAATGGCCACTTCTTGGGGCACAGTCTTTTTCATGCTGGTGGTATCCTGTGTTGCA 300
Qy 301 GCGCTGTCTCCACAGGAACCCAGCAGACTTGGTTTGAGGGTATCTTCTGTCTTCCATGT 360
Db 301 GCGCTGTCTCCACAGGAACCCAGCAGACTTGGTTTGAGGGTATCTTCTGTCTTCCATGT 360
Qy 361 GCGCCATCAATGTGAGCGCCAGCACCTTGTATGGAATTAATGTTGATGAGGGAGCAGCTG 420
Db 361 GCGCCATCAATGTGAGCGCCAGCACCTTGTATGGAATTAATGTTGATGAGGGAGCAGCTG 420
Qy 421 GAACTCGAATTCATGTTTACACCTTTGTGAGAAAAATGCCAGACAGCTTCCAAATCTAG 480
Db 421 GAACTCGAATTCATGTTTACACCTTTGTGAGAAAAATGCCAGACAGCTTCCAAATCTAG 480
Qy 481 AAGGGGAAGTTTGTGAGTCTGTGAGCCAGGACTTCTGCTTTGTAGATCAACCTAAGC 540
Db 481 AAGGGGAAGTTTGTGAGTCTGTGAGCCAGGACTTCTGCTTTGTAGATCAACCTAAGC 540
Qy 541 AGGGTGTGAGACCGTTCAAGGGCTCTTAGAGGTGGCCAAAGACTCAATCCCCGAAGTC 600
Db 541 AGGGTGTGAGACCGTTCAAGGGCTCTTAGAGGTGGCCAAAGACTCAATCCCCGAAGTC 600
Qy 601 ACTGGAAGAACCCAGTGGTCTTAAGGCAACAGCAGGACTACGCTTACTGCCAGAAC 660
Db 601 ACTGGAAGAACCCAGTGGTCTTAAGGCAACAGCAGGACTACGCTTACTGCCAGAAC 660
Qy 661 ACAAAGCCAGGCTCTCTTTGAGGTAAAGGAGATCTTCAGGAAAGTCACTTTCCTGG 720
Db 661 ACAAAGCCAGGCTCTCTTTGAGGTAAAGGAGATCTTCAGGAAAGTCACTTTCCTGG 720
Qy 721 TACCAAAGGGCAGTGTAGCATCATGGATGGATCCGACGAAGGATATTAGCTTGGGTTA 780
Db 721 TACCAAAGGGCAGTGTAGCATCATGGATGGATCCGACGAAGGATATTAGCTTGGGTTA 780
Qy 781 CTGTGAATTTCTGACAGGTCAAGTGCATGGCCACAGACAGGAGACTGTGGGACCTTGG 840
Db 781 CTGTGAATTTCTGACAGGTCAAGTGCATGGCCACAGACAGGAGACTGTGGGACCTTGG 840
Qy 841 ACCTAGGGGAGCCTCCACCAATCACGTTCTGCTGCCAGTTTGAGAAAACTCTGGAAC 900
Db 841 ACCTAGGGGAGCCTCCACCAATCACGTTCTGCTGCCAGTTTGAGAAAACTCTGGAAC 900
Qy 901 AAATCCTAGGGCTACCTCACCTTCTTTCAGATGTTTAAACAGCACTTATAAGCTCTATA 960
Db 901 AAATCCTAGGGCTACCTCACCTTCTTTCAGATGTTTAAACAGCACTTATAAGCTCTATA 960
Qy 961 CACATAGTTACCTGGGATTTGGATTGAAGGTGCAAGACTAGCAACCTGGAGCCCTGG 1020
Db 961 CACATAGTTACCTGGGATTTGGATTGAAGGTGCAAGACTAGCAACCTGGAGCCCTGG 1020
Qy 1021 AGACAGAAGGGACTGATGGGCACACTTTCGAGTGCCTGTTTACCGAGATGGTTGGAAG 1080
Db 1021 AGACAGAAGGGACTGATGGGCACACTTTCGAGTGCCTGTTTACCGAGATGGTTGGAAG 1080
Qy 1081 CAGAGTGGATCTTTGGGGTGTGAAATACCAATACCAATACCAATACCAATACCAATACCA 1140
Db 1081 CAGAGTGGATCTTTGGGGTGTGAAATACCAATACCAATACCAATACCAATACCA 1140
Qy 1141 GCTTTGAGCCCTGCTATGCCGAAGTGTGAGGGTGGTACGAGGAAACTTCACCAGCCAG 1200
Db 1141 GCTTTGAGCCCTGCTATGCCGAAGTGTGAGGGTGGTACGAGGAAACTTCACCAGCCAG 1200
Qy 1201 AGGAGGTCCAGAGAGTTCCTTCTATGCTTCTTCTTACTATTATGACCGAGCTGTTGACA 1260
Db 1201 AGGAGGTCCAGAGAGTTCCTTCTATGCTTCTTCTTACTATTATGACCGAGCTGTTGACA 1260
Qy 1261 CAGACATGATTGATTATGAAGAGGGGGTATTTTAAAGTTGAAGATTTTGAAGAAAAAG 1320

1261 CAGACATGATTGATTATGAAAGGGGGTATT-TAAAGTTGAAGATTTGAAAGAAAG 1320
1321 CCAGGGAAGTGTGTGATAACTTGGAAAACTTACCTCAGGCAGTCTTCTGTGCAATGG 1380
1321 CCAGGGAAGTGTGTGATAACTTGGAAAACTTACCTCAGGCAGTCTTCTGTGCAATGG 1380
1381 ATCTCAGCTACATCAGACCCCTGTTAAAGGATGGCTTTGGCTTTGCAGACGACAGTCT 1440
1381 ATCTCAGCTACATCAGACCCCTGTTAAAGGATGGCTTTGGCTTTGCAGACGACAGTCT 1440
1441 TACAG 1445
1441 TACAG 1445

RESULT 8
S-09-557-800C-24
Sequence 24, Application US/09557800C
Patent No. 6476211
GENERAL INFORMATION:
APPLICANT: Ford, John
APPLICANT: Mulero, Julio
APPLICANT: Yeung, George
TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 28110/36457
CURRENT APPLICATION NUMBER: US/09/557,800C
CURRENT FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/481,238
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: 09/370,265
PRIOR FILING DATE: 1999-08-09
PRIOR APPLICATION NUMBER: PCT/US99/16180
PRIOR FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: 09/350836
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 09/273447
PRIOR FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: 09/122449
PRIOR FILING DATE: 1998-07-24
PRIOR APPLICATION NUMBER: 09/244444
PRIOR FILING DATE: 1999-02-04
PRIOR APPLICATION NUMBER: 09/118,205
PRIOR FILING DATE: 1998-07-16
NUMBER OF SEQ ID NOS: 56
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 24
LENGTH: 1601
TYPE: DNA
ORGANISM: Homo sapiens
S-09-557-800C-24

Query Match 80.3%; Score 1445; DB 4; Length 1601;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 GCGGGCTGCCGCGCAAGGTGGCGCGCGCGGTTTCCCTTGTTCCTGTGTCACAAAGAAA 60
1 GCGGGCTGCCGCGCAAGGTGGCGCGCGCGGTTTCCCTTGTTCCTGTGTCACAAAGAAA 60
61 TGTGGAGTGTCTTGGCTGAATCCTCATACAGACAAGATCATTATGGTGTCTTAGGTTGA 120
61 TGTGGAGTGTCTTGGCTGAATCCTCATACAGACAAGATCATTATGGTGTCTTAGGTTGA 120
121 AAAAGTGATATAATAAGGAACCAAGGAGAAAATTGAGAGGAAAGAAAATAATTCCTCT 180
121 AAAAGTGATATAATAAGGAACCAAGGAGAAAATTGAGAGGAAAGAAAATAATTCCTCT 180
181 GCAGGTGTGCGAGCAGGATTCCTTCTGCAACAAGAGCCCTCCACCCAGCCACATCTTGGGA 240
181 GCAGGTGTGCGAGCAGGATTCCTTCTGCAACAAGAGCCCTCCACCCAGCCACATCTTGGGA 240
241 AAAGAAATGGCCACTCTTGGGGGCACAGTCTTTTTCATGCTGGTGGTATCCTGTGTTGCA 300

Db 241 AAAGAATGGCCACTTCTTTGGGCACAGTCTTTTTCATGCTGGTGGTATCCTGTGTTGCA 300
QY 301 GCGTGTCTCCACAGGAACACAGACACTTGGTTTGAGGGTATCTTCTGTCTTCCATGT 360
Db 301 GCGTGTCTCCACAGGAACACAGACACTTGGTTTGAGGGTATCTTCTGTCTTCCATGT 360
QY 361 GCGCCATCAATGTCAAGCCAGACACCTTGTATGGAATATGTTTGTATGCAGGGAGCACTG 420
Db 361 GCGCCATCAATGTCAAGCCAGACACCTTGTATGGAATATGTTTGTATGCAGGGAGCACTG 420
QY 421 GAACTCGAATTCATGTTTACACCTTTGTGCAGAAAATGCCAGGACAGCTTCCAATTCTAG 480
Db 421 GAACTCGAATTCATGTTTACACCTTTGTGCAGAAAATGCCAGGACAGCTTCCAATTCTAG 480
QY 481 AAGGGGAAGTTTTTGAATCTGTGAAGCCAGGACTTTTCTGCTTTTGTAGATCAACCTAAGC 540
Db 481 AAGGGGAAGTTTTTGAATCTGTGAAGCCAGGACTTTTCTGCTTTTGTAGATCAACCTAAGC 540
QY 541 AGGCTGCTGAGACCGTTCAAGGGCTCTTAGAGGTGGCCAAAAGACTCAATCCCCCGAAGTC 600
Db 541 AGGCTGCTGAGACCGTTCAAGGGCTCTTAGAGGTGGCCAAAAGACTCAATCCCCCGAAGTC 600
QY 601 ACTGGAAAAAGACCCCGAGTGGTCTTAAAGGCAACAGCAGGACTACGCTTACTGCCAGAAC 660
Db 601 ACTGGAAAAAGACCCCGAGTGGTCTTAAAGGCAACAGCAGGACTACGCTTACTGCCAGAAC 660
QY 661 ACMAAGCCAAAGGCTCTGCTCTTTGAGGTAAAGGAGATCTTTCAGGAAGTCACTTTCCTGG 720
Db 661 ACMAAGCCAAAGGCTCTGCTCTTTGAGGTAAAGGAGATCTTTCAGGAAGTCACTTTCCTGG 720
QY 721 TACCAAGGGCAGTGTAGCATCATGGATGGATCCGACCAAGGCATATTAGCTTGGTTA 780
Db 721 TACCAAGGGCAGTGTAGCATCATGGATGGATCCGACCAAGGCATATTAGCTTGGTTA 780
QY 781 CTGTGAATTTCTGACAGGTCAAGTGCATGGCCACACAGCAGGACTGTGGGACCTTGG 840
Db 781 CTGTGAATTTCTGACAGGTCAAGTGCATGGCCACACAGCAGGACTGTGGGACCTTGG 840
QY 841 ACCTAGGGGGAGCCTCCACCCAAATCACGTTCCCTGCCCCAGTTTGAGAAAACCTTGGAAAC 900
Db 841 ACCTAGGGGGAGCCTCCACCCAAATCACGTTCCCTGCCCCAGTTTGAGAAAACCTTGGAAAC 900
QY 901 AAACTCCTAGGGGCTACCTCACCTTCTTTGAGATGTTTAAACAGCACTTATAAGCTCTATA 960
Db 901 AAACTCCTAGGGGCTACCTCACCTTCTTTGAGATGTTTAAACAGCACTTATAAGCTCTATA 960
QY 961 CACATAGTTTACCTGGGATTTGGATTGAAAGCTGCAAGACTAGCAACCTTGGGAGCCTGG 1020
Db 961 CACATAGTTTACCTGGGATTTGGATTGAAAGCTGCAAGACTAGCAACCTTGGGAGCCTGG 1020
QY 1021 AGACAGAAGGGACTGATGGGCACACTTTCCGGAGTGCCTGTTTACCGAGATGTTGGAAAG 1080
Db 1021 AGACAGAAGGGACTGATGGGCACACTTTCCGGAGTGCCTGTTTACCGAGATGTTGGAAAG 1080
QY 1081 CAGAGTGGATCTTTGGGGTGTGAAATACCAGTATGTGGGCAACCAAGAGGGGAGGTGG 1140
Db 1081 CAGAGTGGATCTTTGGGGTGTGAAATACCAGTATGTGGGCAACCAAGAGGGGAGGTGG 1140
QY 1141 GCTTTGAGCCCTGCTATGCCGAAGTCTGAGGGTGGTACGAGGAAACCTTACCAGCCAG 1200
Db 1141 GCTTTGAGCCCTGCTATGCCGAAGTCTGAGGGTGGTACGAGGAAACCTTACCAGCCAG 1200
QY 1201 AGGAGGTCCAGAGAGGTCTTCTATGCTTTCTTCTTACTATTATGACCGAGCTGTTGACA 1260
Db 1201 AGGAGGTCCAGAGAGGTCTTCTATGCTTTCTTCTTACTATTATGACCGAGCTGTTGACA 1260
QY 1261 CAGACATGATTGATTATGAAAAGGGGGTATTTTAAAGTTGAAGATTTGAAAAGAAAAG 1320
Db 1261 CAGACATGATTGATTATGAAAAGGGGGTATTTTAAAGTTGAAGATTTGAAAAGAAAAG 1320
QY 1321 CCAGGGAAGTGTGTGATAACTTGGAAAACCTTCACTCAGGCAGTCTTCTTCTGTCATGG 1380

b 1321 CCAGGGAAGTGTGTGATAACTTGGAAAACTTCACCTCAGGCAGTCCTTTCCCTGTGCATGG 1380
Y 1381 ATCTCAGCTACATCACAGCCCTGTGTTAAAGGATGGCTTTGGCTTTGCAGACAGCACAGTCT 1440
D 1381 ATCTCAGCTACATCACAGCCCTGTGTTAAAGGATGGCTTTGGCTTTGCAGACAGCACAGTCT 1440
Y 1441 TACAG 1445
b 1441 TACAG 1445

RESULT 9
S-09-608-285A-4
Sequence 4, Application: US/09508285A
Patent No. 6335013
GENERAL INFORMATION:
APPLICANT: Ford, John
APPLICANT: Mulero, Julio
APPLICANT: Yeung, George
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
TITLE OF INVENTION: POLYPEPTIDES
FILE REFERENCE: 28110/36570
CURRENT APPLICATION NUMBER: US/09/608,285A
CURRENT FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 09/583,231
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 09/557,800
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/481,238
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: 09/370,265
PRIOR FILING DATE: 1999-08-09
PRIOR APPLICATION NUMBER: PCT/US99/16180
PRIOR FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: 09/350,836
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 09/273,447
PRIOR FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: 09/244,444
PRIOR FILING DATE: 1999-02-04
PRIOR APPLICATION NUMBER: 09/122,449
PRIOR FILING DATE: 1998-07-24
PRIOR APPLICATION NUMBER: 09/118,205
PRIOR FILING DATE: 1998-07-16
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 1287
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1284)
S-09-608-285A-4

Query Match
Best Local Similarity 71.5%; Score 1287; DB 4; Length 1287;
Matches 1287; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 246 ATGGCCACTTCTTGGGGCAGAGTCTTTTCATGCTGGTGGTATCCTGTGTTTSCAGCGCT 305
b 1 ATGGCCACTTCTTGGGGCAGAGTCTTTTCATGCTGGTGGTATCCTGTGTTTSCAGCGCT 60
Y 306 GTCTCCACAGGAACCCAGCAGACTTGGTTTGAGGGTATCTTCCCTGTCTTCCATGTGCCCC 365
D 61 GTCTCCACAGGAACCCAGCAGACTTGGTTTGAGGGTATCTTCCCTGTCTTCCATGTGCCCC 120
Y 366 ATCAATGTCAGCGCCAGCAGCTTGTATGGAATTATGTTGATGCAGGGAGCACTGGAACT 425
b 121 ATCAATGTCAGCGCCAGCAGCTTGTATGGAATTATGTTGATGCAGGGAGCACTGGAACT 180
Y 426 CGAATTTCATGTTTACACCTTTGTGCAGAAAATGCCAGGACAGCTTCCAAATTCAGAGGG 485

Db 181 CGAATTCATGTTTACACCTTTGTGCAGAAAATGCCAGGACAGCTTCCAAATTCAGAGGG 240
QY 486 GAAGTTTTGATTCTGTGAAGCCAGGACTTTTCTGCTTTTGTAGATCAACCTTAAGCAGGGT 545
Db 241 GAAGTTTTGATTCTGTGAAGCCAGGACTTTTCTGCTTTTGTAGATCAACCTTAAGCAGGGT 300
QY 546 GCTGAGACCGTTCAAGGGCTCTTTAGAGGTGGCCAAAGACTCAATCCCCCGAAGTCACTGG 605
Db 301 GCTGAGACCGTTCAAGGGCTCTTTAGAGGTGGCCAAAGACTCAATCCCCCGAAGTCACTGG 360
QY 606 AAAAAGACCCAGTGGTCCCTAAAGGCAACAGCAGGACTACGCTTACTGCCAGAACACAAA 665
Db 361 AAAAAGACCCAGTGGTCCCTAAAGGCAACAGCAGGACTACGCTTACTGCCAGAACACAAA 420
QY 666 GCCAAGGCTCTGCTCTTTGAGGTAAAGGAGATCTTCAGGAAGTCACCTTTCCTGGTACCA 725
Db 421 GCCAAGGCTCTGCTCTTTGAGGTAAAGGAGATCTTCAGGAAGTCACCTTTCCTGGTACCA 480
QY 726 AAGGSCAGTGTTAGCATCATGGATGGATCCGACGGAAGGCATATTAGCTTGGGTACTGTG 785
Db 481 AAGGSCAGTGTTAGCATCATGGATGGATCCGACGGAAGGCATATTAGCTTGGGTACTGTG 540
QY 786 AATTTTCTGACAGGTCAGCTGCATGGCCACAGACAGGAGACTGTGGGACCTTGGACCTA 845
Db 541 AATTTTCTGACAGGTCAGCTGCATGGCCACAGACAGGAGACTGTGGGACCTTGGACCTA 600
QY 846 GGGGAGCCTCCACCCAAATCAGTTCTCTGCCCTGCTGAGAAAACCTCTGGAACAAACT 905
Db 601 GGGGAGCCTCCACCCAAATCAGTTCTCTGCCCTGCTGAGAAAACCTCTGGAACAAACT 660
QY 906 CTTAGGGGCTACCTCAGTTCTGAGATGTTTAAAGCACTTATAAGCTCTATACACAT 965
Db 661 CTTAGGGGCTACCTCAGTTCTGAGATGTTTAAAGCACTTATAAGCTCTATACACAT 720
QY 966 AGTTACCTGGGATTGGATTGAAAGCTGCAAGACTAGCAACCCCTGGGAGCCCTGGAGACA 1025
Db 721 AGTTACCTGGGATTGGATTGAAAGCTGCAAGACTAGCAACCCCTGGGAGCCCTGGAGACA 780
QY 1026 GAAGGACTGATGGGCACACTTCCGGAGTGCTGTTTACCGAGATGTTGGGAAGCAGAG 1085
Db 781 GAAGGACTGATGGGCACACTTCCGGAGTGCTGTTTACCGAGATGTTGGGAAGCAGAG 840
QY 1086 TGGATCTTTGGGGTGTAATACCAAGTATGGTGGCAACCAAGAGGGGAGGTGGCTTT 1145
Db 841 TGGATCTTTGGGGTGTAATACCAAGTATGGTGGCAACCAAGAGGGGAGGTGGCTTT 900
QY 1146 GAGCCTGCTATGCCGAAGTCTGAGGGTGGTACGAGGAAAACCTTCACCAGCCAGAGAG 1205
Db 901 GAGCCTGCTATGCCGAAGTCTGAGGGTGGTACGAGGAAAACCTTCACCAGCCAGAGAG 960
QY 1206 GTCCAGAGAGGTTCCCTCTATGCTTTCTCTTACTATTATGACCGAGCTGTTGACACAGAC 1265
Db 961 GTCCAGAGAGGTTCCCTCTATGCTTTCTCTTACTATTATGACCGAGCTGTTGACACAGAC 1020
QY 1266 ATGATTGATTATGAAAAGGGGGTATTTTAAAGTTGAAGATTTTGAAGAAAAGCCAGG 1325
Db 1021 ATGATTGATTATGAAAAGGGGGGTATTTTAAAGTTGAAGATTTTGAAGAAAAGCCAGG 1080
QY 1326 GAAGTGTGTGATAAATCTTGGAAAACCTTCACCTCAGGAGTCCCTTCCCTGTGCAATGATCTC 1385
Db 1081 GAAGTGTGTGATAAATCTTGGAAAACCTTCACCTCAGGAGTCCCTTCCCTGTGCAATGATCTC 1140
QY 1386 AGCTACATCACAGCCCTGTAAAGGATGGCTTTGGCTTTGCAGACAGCAGACTCTTACAG 1445
Db 1141 AGCTACATCACAGCCCTGTAAAGGATGGCTTTGGCTTTGCAGACAGCAGACTCTTACAG 1200
QY 1446 CTCAAAAAGAAAGTGAACAACATAGAGACGGGCTTGGGCCCTTGGGGGCCACCTTTCACCTG 1505
Db 1201 CTCAAAAAGAAAGTGAACAACATAGAGACGGGCTTGGGCCCTTGGGGGCCACCTTTCACCTG 1260
QY 1506 TTGCAGTCTCTGGGCATCTCCCATTTGA 1532
Db 1261 TTGCAGTCTCTGGGCATCTCCCATTTGA 1287

RESULT 10
S-09-350-836B-4

Sequence 4, Application US/09350836B
Patent No. 6387645

GENERAL INFORMATION:

APPLICANT: Ford, John
APPLICANT: Mulero, Julio
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
TITLE OF INVENTION: POLYPEPTIDES
FILE REFERENCE: 28110/35761

CURRENT APPLICATION NUMBER: US/09/350,836B

CURRENT FILING DATE: 1999-07-09

PRIOR APPLICATION NUMBER: 09/273,447

PRIOR FILING DATE: 1999-03-19

PRIOR APPLICATION NUMBER: 09/118,205

PRIOR FILING DATE: 1998-07-16

PRIOR APPLICATION NUMBER: 09/122,449

PRIOR FILING DATE: 1998-07-24

PRIOR APPLICATION NUMBER: 09/244,444

PRIOR FILING DATE: 1999-02-04

NUMBER OF SEQ ID NOS: 23

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 4

LENGTH: 1287

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (1)..(1284)

S-09-350-836B-4

Query Match 71.5%; Score 1287; DB 4; Length 1287;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1287; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

246 ATGGCCACTTCTTGGGGCACAGTCTTTTTCATGCTGGTGGTATCCCTGTGTTTCAGCGCT 305
1 ATGGCCACTTCTTGGGGCACAGTCTTTTTCATGCTGGTGGTATCCCTGTGTTTCAGCGCT 60
306 GTCTCCACAGGAACACAGACTTGGTTGAGGGTATCTTCCCTGCTTCCATGTGCCCC 365
61 GTCTCCACAGGAACACAGACTTGGTTGAGGGTATCTTCCCTGCTTCCATGTGCCCC 120
366 ATCAATGTCAGCGCCAGCACCTTGTATGGAATTATGTTTGTATGTCAGGAGCACTGGAAC 425
121 ATCAATGTCAGCGCCAGCACCTTGTATGGAATTATGTTTGTATGTCAGGAGCACTGGAAC 180
426 CGAATTCATGTTTACACCTTTGTGCAGAAAATGCCAGGACAGCTTCCCAATCTAGAAAGG 485
181 CGAATTCATGTTTACACCTTTGTGCAGAAAATGCCAGGACAGCTTCCCAATCTAGAAAGG 240
486 GAAGTTTTTGTATCTGTGAAGCCAGGACTTTCTGCTTTTGTAGATCAACCTAAGCAGGGT 545
241 GAAGTTTTTGTATCTGTGAAGCCAGGACTTTCTGCTTTTGTAGATCAACCTAAGCAGGGT 300
546 GCTGAGACCGTTCAAGGGCTCTTAGAGGTGGCCAAAGACTCAATCCCGGAAGTCACTGG 605
301 GCTGAGACCGTTCAAGGGCTCTTAGAGGTGGCCAAAGACTCAATCCCGGAAGTCACTGG 360
606 AAAAAGACCCCGAGTCTCTAAAGGCAACAGCAGGACTACGCTTACTGCCAGAACACAAA 665
361 AAAAAGACCCCGAGTCTCTAAAGGCAACAGCAGGACTACGCTTACTGCCAGAACACAAA 420
666 GCCAAGGCTCTGCTCTTTGAGGTAAGGAGATCTTCAGGAAGTCACCTTTCTGTTACCA 725
421 GCCAAGGCTCTGCTCTTTGAGGTAAGGAGATCTTCAGGAAGTCACCTTTCTGTTACCA 480
726 AAGGGCAGTGTTAGCATCATGGATGGATCCGACGAAGGCATATTAGCTTGGTTACTGTG 785
481 AAGGGCAGTGTTAGCATCATGGATGGATCCGACGAAGGCATATTAGCTTGGTTACTGTG 540

QY 786 AATTTTCTGACAGGTCACTGCTATGGCCACAGACAGGAGACTGTGGGACCTTGGACCTA 845
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
541 AATTTTCTGACAGGTCACTGCTATGGCCACAGACAGGAGACTGTGGGACCTTGGACCTA 600
QY 846 GGGGAGCCTCCACCCAAATCACGTTCTGCCCCAGTTTGAGAAAACCTCTGGAACAACT 905
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
601 GGGGAGCCTCCACCCAAATCACGTTCTGCCCCAGTTTGAGAAAACCTCTGGAACAACT 660
QY 906 CCTAGGGGCTACCTCACTTCTCTTTGAGATGTTTAAAGCTTATAAGCTCTATACACAT 965
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
661 CCTAGGGGCTACCTCACTTCTCTTTGAGATGTTTAAAGCTTATAAGCTCTATACACAT 720
QY 966 AGTTACCTGGGATTGGATTGAAAGCTGCAAGACTAGCAACCTCTGGAGCCCTGGAGACA 1025
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
721 AGTTACCTGGGATTGGATTGAAAGCTGCAAGACTAGCAACCTCTGGAGCCCTGGAGACA 780
QY 1026 GAAGGACTGATGGGCACACTTTCGGGAGTGCTTACCGAGATGGTTGGAGCAGAG 1085
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781 GAAGGACTGATGGGCACACTTTCGGGAGTGCTTACCGAGATGGTTGGAGCAGAG 840
QY 1086 TCGATCTTTGGGGGTGGAATACCAATACCAATACCAATACCAATACCAATACCAAT 1145
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
841 TCGATCTTTGGGGGTGGAATACCAATACCAATACCAATACCAATACCAATACCAAT 900
QY 1146 GAGCCCTGCTATGCCGAAGTCTGAGGGTGGTACGAGGAAACCTTCAACGACGAGGAG 1205
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
901 GAGCCCTGCTATGCCGAAGTCTGAGGGTGGTACGAGGAAACCTTCAACGACGAGGAG 960
QY 1206 GTCCAGAGAGGTTCTTCTATGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1265
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
961 GTCCAGAGAGGTTCTTCTATGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1020
QY 1266 ATGATTGATTATGAAAAGGGGGTATTTTAAAGTTGAAGATTTTGAAGAAAAGCCAGG 1325
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1021 ATGATTGATTATGAAAAGGGGGTATTTTAAAGTTGAAGATTTTGAAGAAAAGCCAGG 1080
QY 1326 GAAGTGTGTGATAACTTGGAAAACCTTCACTCAGSCAGTCTTCTTCTGTCATGATCTC 1385
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QY 1386 AGCTACATCACAGCCCTGTTAAAGGATGGCTTTGGCTTTGCAGACAGCAGCTCTTACAG 1445
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1141 AGCTACATCACAGCCCTGTTAAAGGATGGCTTTGGCTTTGCAGACAGCAGCTCTTACAG 1200
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Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1201 CTCACAAAAGAAAGTGAACAACATAGAGACGGGCTTGGGCTTGGGGCCACCTTTTACCTG 1260
QY 1506 TTGCAGTCTCTGGGCATCTCCCATTTGA 1532
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1261 TTGCAGTCTCTGGGCATCTCCCATTTGA 1287

RESULT 11

US-09-370-265-4

; Sequence 4, Application US/09370265

; Patent No. 644771

; GENERAL INFORMATION:

; APPLICANT: Ford, John

; APPLICANT: Mulero, Julio

; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE

; TITLE OF INVENTION: POLYPEPTIDES

; FILE REFERENCE: 28111/35908

; CURRENT APPLICATION NUMBER: US/09/370,265

; CURRENT FILING DATE: 1999-08-09

; EARLIER APPLICATION NUMBER: PCT/US99/16180

; EARLIER FILING DATE: 1999-07-16

; EARLIER APPLICATION NUMBER: 09/350,836

; EARLIER FILING DATE: 1999-07-09

; EARLIER APPLICATION NUMBER: 09/273,447

; EARLIER FILING DATE: 1999-03-19

; EARLIER APPLICATION NUMBER: 09/244,444

; EARLIER FILING DATE: 1999-02-04

EARLIER APPLICATION NUMBER: 09/122,449
EARLIER FILING DATE: 1998-07-24
EARLIER APPLICATION NUMBER: 09/118,205
EARLIER FILING DATE: 1998-07-16
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PatentIn ver. 2.0

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SEQ ID NO 4
LENGTH: 1287
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1284)
S-09-370-265-4

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Query Match 71.5%; Score 1287; DB 4; Length 1287;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1287; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

246	ATGGCCACTTCTTGGGGCAGATCTTTTTCATGCTGGTGGTATCCTGTGTTTGCAGCGGT	305
1	ATGGCCACTTCTTGGGGCAGATCTTTTTCATGCTGGTGGTATCCTGTGTTTGCAGCGGT	60
306	GTCTCCACAGGAACCCAGCAGACTTGGTTTGAGGGTATCTTCCCTGTCTTCCATGTGCCCC	365
61	GTCTCCACAGGAACCCAGCAGACTTGGTTTGAGGGTATCTTCCCTGTCTTCCATGTGCCCC	120
366	ATCAATGTTCAGCGCCAGCACTTGTATGGAATATGTTTGATGCAGGGAGCCTGGAACT	425
121	ATCAATGTTCAGCGCCAGCACTTGTATGGAATATGTTTGATGCAGGGAGCCTGGAACT	180
426	CGAATTTCATGTTTACACCTTTGTGCAGAAAAATGCCAGGACAGCTTCCAATTCTAGAGGG	485
181	CGAATTTCATGTTTACACCTTTGTGCAGAAAAATGCCAGGACAGCTTCCAATTCTAGAGGG	240
486	GAAGTTTTTGATTCTGTGAAGCCAGGACTTTCTGCTTTTGTAGATCAACCTAAGCAGGGT	545
241	GAAGTTTTTGATTCTGTGAAGCCAGGACTTTCTGCTTTTGTAGATCAACCTAAGCAGGGT	300
546	GCTGAGACCGTTCAAGGGCTCTTTAGAGGTGGCCAAAGACTCAATCCCCCGAAGTCACTGG	605
301	GCTGAGACCGTTCAAGGGCTCTTTAGAGGTGGCCAAAGACTCAATCCCCCGAAGTCACTGG	360
606	AAAAAGACCCCGTGGTCTTAAAGGCAACAGCAGGACTACGTTACTGCCAGAACACAA	665
361	AAAAAGACCCCGTGGTCTTAAAGGCAACAGCAGGACTACGTTACTGCCAGAACACAA	420
666	GCCAAAGGCTCTGCTCTTTGAGGTAAAGGAGATCTTCAGGAAGTCACTTTCCTGGTACCA	725
421	GCCAAAGGCTCTGCTCTTTGAGGTAAAGGAGATCTTCAGGAAGTCACTTTCCTGGTACCA	480
726	AAGGGCAGTGTTAGCATCATGGATGGATCCGACGAAGGCATATTAGCTTTGGTTACTGTG	785
481	AAGGGCAGTGTTAGCATCATGGATGGATCCGACGAAGGCATATTAGCTTTGGTTACTGTG	540
786	AATTTTCTGACAGGTCAGCTGCATGGCCACAGACAGGAGACTGTGGGACCTTGGACCTA	845
541	AATTTTCTGACAGGTCAGCTGCATGGCCACAGACAGGAGACTGTGGGACCTTGGACCTA	600
846	GGGGGAGCCTCCACCCCAATCAGCTTCCCTGCCCCAGTTTGAGAAAATCTCTGGAACAACT	905
601	GGGGGAGCCTCCACCCCAATCAGCTTCCCTGCCCCAGTTTGAGAAAATCTCTGGAACAACT	660
906	CCTAGGGGCTACCTCAGCTTCCCTTGAGATGTTTAAACAGCATTATTAAGCTCTATACACT	965
661	CCTAGGGGCTACCTCAGCTTCCCTTGAGATGTTTAAACAGCATTATTAAGCTCTATACACT	720
966	AGTTACCTGGGATTTGGATTGAAAGCTGCAAGACTAGCAACCTGGGAGCCCTGGAGACA	1025
721	AGTTACCTGGGATTTGGATTGAAAGCTGCAAGACTAGCAACCTGGGAGCCCTGGAGACA	780
1026	GAAGGGACTGATGGGCACACTTTCGGAGTGCCTGTTTACCGAGATGGTTGGAAGCAGAG	1085

us-09-557-800C-4

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Query Match      71.5%; Score 1287; DB 4; Length 1287;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1287; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

246 ATGGCCACTTCTTGGGGCACAGTCTTTTTCATGCTGGTGGTATCCTGTGTTTGCACGGCT 305
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1 ATGGCCACTTCTTGGGGCACAGTCTTTTTCATGCTGGTGGTATCCTGTGTTTGCACGGCT 60
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306 GTCTCCACAGGAACACAGACTTGGTTTGAGGGTATCTTCTGTCTTCCATGTGCCCC 365
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61 GTCTCCACAGGAACACAGACTTGGTTTGAGGGTATCTTCTGTCTTCCATGTGCCCC 120
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366 ATCAATGTACGCCACAGCACTTGTATGGAATTATGTTTGATGAGGGAGCACTGGAAC 425
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121 ATCAATGTACGCCACAGCACTTGTATGGAATTATGTTTGATGAGGGAGCACTGGAAC 180
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426 CGAATTCATGTTTACACCTTGTGCAAGAAATGCCAGGACAGCTTCCAATTCTAGAAGG 485
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181 CGAATTCATGTTTACACCTTGTGCAAGAAATGCCAGGACAGCTTCCAATTCTAGAAGG 240
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486 GAAGTTTTCATCTGTAAGCCAGGACTTCTGCTTTTGTAGATCAACCTAAGCAGGGT 545
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241 GAAGTTTTCATCTGTAAGCCAGGACTTCTGCTTTTGTAGATCAACCTAAGCAGGGT 300
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546 GCTGAGACCGTTCAAGGGCTCTTAGAGGTGGCCCAAGACTCAATCCCGCCGAAGTCACTGG 605
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301 GCTGAGACCGTTCAAGGGCTCTTAGAGGTGGCCCAAGACTCAATCCCGCCGAAGTCACTGG 360
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606 AAAAGACCCCACTGGTCTTAAGGCAACAGCAGGACTACGCTTACTGCCAGAACACAAA 665
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421 GCAAAGGCTGCTGCTTTGAGGTAAAGAGATCTTCAGGAAGTCACTTTCCTGGTACCA 480
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726 AAGGGCAGTGTAGCATCATGGATGGATCCGACGAAGGCATATTAGCTTGGTTACTGTG 785
|||||
481 AAGGGCAGTGTAGCATCATGGATGGATCCGACGAAGGCATATTAGCTTGGTTACTGTG 540
|||||

786 AATTTTCTGACAGGTCAGCTGCATGGCCACAGACAGGAGACTGTGGGACCTTGGACCTA 845
|||||
541 AATTTTCTGACAGGTCAGCTGCATGGCCACAGACAGGAGACTGTGGGACCTTGGACCTA 600
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846 GGGGGAGCTCCACCCCAATCACGTTCTGCCCCCAGTTTGAGAAAACCTCTGGAACAACT 905
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601 GGGGGAGCTCCACCCCAATCACGTTCTGCCCCCAGTTTGAGAAAACCTCTGGAACAACT 660
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906 CCTAGGGGTACCTCACTTCTTTGAGATGTTTAAACAGCACTTATAAGCTCTATACACAT 965
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661 CCTAGGGGTACCTCACTTCTTTGAGATGTTTAAACAGCACTTATAAGCTCTATACACAT 720
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966 AGTTACCTGGGATTTGATTGAAAGCTGCAAGACTAGCAACCCCTGGGAGCCCTGGAGACA 1025
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721 AGTTACCTGGGATTTGATTGAAAGCTGCAAGACTAGCAACCCCTGGGAGCCCTGGAGACA 780
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1026 GAAGGGACTGTAGGGCACACTTTCGGGAGTGCCTGTTTACCGAGATGGTTGGAAGCAGAG 1085
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781 GAAGGGACTGTAGGGCACACTTTCGGGAGTGCCTGTTTACCGAGATGGTTGGAAGCAGAG 840
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1086 TGGATCTTTGGGGGTGTGAATACCAAGTATGGTGGCAACCAAGAGGGGAGGTGGGCTTT 1145
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1146 GAGCCCTGCTATGCCGAAGTGTCTGAGGGTGGTACGAGGAAACTTCAACGAGCCAGAGGAG 1205
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901 GAGCCCTGCTATGCCGAAGTGTCTGAGGGTGGTACGAGGAAACTTCAACGAGCCAGAGGAG 960
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1206 GTCCAGAGAGGTTCTCTTCTATGCTTTCTCTTACTATTATGACCGAGCTGTTGACACAGAC 1265
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961 GTCCAGAGAGGTTCTCTTCTATGCTTTCTCTTACTATTATGACCGAGCTGTTGACACAGAC 1020
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QY      1266 ATGATTGATTATGAAAAGGGGGGTATTTTAAAGTTGAAGATTTTGAAGAAAAGCCAGG 1325
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DB      1021 ATGATTGATTATGAAAAGGGGGGTATTTTAAAGTTGAAGATTTTGAAGAAAAGCCAGG 1080
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QY      1326 GAAGTGTGTGATAACTTGGAAAACCTTCAACCTCAGGCAGTCCCTTTCCTGTGATGGATCTC 1385
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DB      1081 GAAGTGTGTGATAACTTGGAAAACCTTCAACCTCAGGCAGTCCCTTTCCTGTGATGGATCTC 1140
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QY      1386 AGCTACATCACAGCCCTGTTAAAGGATGGCTTTGGCTTTGCAGACAGCAGACTCTTACAG 1445
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DB      1141 AGCTACATCACAGCCCTGTTAAAGGATGGCTTTGGCTTTGCAGACAGCAGACTCTTACAG 1200
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QY      1446 CTCACAAAGAAAGTGAACAACATAGAGACGGGCTGGGCTTGGGGGCCACCTTTTACCTG 1505
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DB      1201 CTCACAAAGAAAGTGAACAACATAGAGACGGGCTGGGCTTGGGGGCCACCTTTTACCTG 1260
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QY      1506 TTGCAGTCTCTGGGCATCTCCCAATTGA 1532
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DB      1261 TTGCAGTCTCTGGGCATCTCCCAATTGA 1287
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RESULT 13
US-09-608-285A-6
; Sequence 6, Application US/09608285A
; Patent No. 6335013
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 28110/36570
; CURRENT APPLICATION NUMBER: US/09/608,285A
; CURRENT FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/583,231
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 09/557,800
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn, Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1287
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1284)
US-09-608-285A-6

Query Match      71.0%; Score 1277.4; DB 4; Length 1287;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1281; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      246 ATGGCCACTTCTTGGGGCACAGTCTTTTTCATGCTGGTGGTATCCTGTGTTTGCACGGCT 305
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DB      1 ATGGCCACTTCTTGGGGCACAGTCTTTTTCATGCTGGTGGTATCCTGTGTTTGCACGGCT 60
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306 GTCTCCACAGGAACACGACACTTGGTTTGAGGTATCTTCCTGCTCCATGTGCCCC 365
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61 GTCTCCACAGGAACACGACACTTGGTTTGAGGTATCTTCCTGCTCCATGTGCCCC 120
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366 ATCAATGTGAGCGCCAGACCTTGTATGGAATTATGTTTGATGAGGAGCACTGGAACT 425
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426 CGAATTTCATGTTTACACCTTTGTGCAGAAAATGCGAGACAGCTTCCAAATCTAGAAGG 485
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181 CGAATTTCATGTTTACACCTTTGTGCAGAAAATGCCAGGACAGCTTCCAAATCTAGAAGG 240
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QY 1386 AGCTACATCACAGCCCTGTTAAAGGATGGCTTTGGCTTTGCAGACAGCAGTCTTACAG 1445
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QY 1446 CTCACAAAGAAAGTGAACAACATAGAGACGGGCTGGCCCTTGGGGGCCACCTTTACACCTG 1505
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DB 1201 CTCACAAAGAAAGTGAACAACATAGAGACGGGCTGGCCCTTGGGGGCCACCTTTACACCTG 1260
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DB 1261 TTGCAGTCTCTGGGCATCTCCCATTTGA 1287
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RESULT 14
US-09-350-836B-6
; Sequence 6, Application US/09350836B
; Patent No. 6387645
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 28110/35761
; CURRENT APPLICATION NUMBER: US/09/350,836B
; CURRENT FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1287
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1284)
US-09-350-836B-6

Query Match 71.0%; Score 1277.4; DB 4; Length 1287;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 128; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 246 ATGCCACTTCTTGGGGCACAGTCTTTTTCATGCTGGTGGTATCCTGTGTTTGCAGCGCT 305
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DB 1 ATGCCACTTCTTGGGGCACAGTCTTTTTCATGCTGGTGGTATCCTGTGTTTGCAGCGCT 60
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QY 306 GTCTCCACAGGAACCGACAGACTTGGTTTGAGGTATCTTCCTGTCTTCCATGTGCCCC 365
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QY 366 ATCAATGTCAGCGCCAGCACTTGTATGGAATTATGTTTGATGCAGGAGCACTGGAACT 425
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DB 121 ATCAATGTCAGCGCCAGCACTTGTATGGAATTATGTTTGATGCAGGAGCACTGGAACT 180
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QY 426 CGAATTCATGTTTACACCTTTGTGCAGAAAATGCCAGSACAGCTTCCAAATCTAGAAGGG 485
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DB 181 CGAATTCATGTTTACACCTTTGTGCAGAAAATGCCAGSACAGCTTCCAAATCTAGAAGGG 240
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DB 241 GAAGTTTCTGATTCTGTGAAGCCAGGACTTTCTGCTTTGTAGATCAACCTAAGCAGGGT 300
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QY 546 GCTGAGACCGTTCAAGGGCTCTTAGAGGTGGCCAAAGACTCAATCCCCCGAAGTCACTGG 605
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DB 301 GCTGAGACCGTTCAAGGGCTCTTAGAGGTGGCCAAAGACTCAATCCCCCGAAGTCACTGG 360
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RESULT 15

3-09-370-265-6

Sequence 6, Application US/09370265

Patent No. 6447771

GENERAL INFORMATION:

APPLICANT: Ford, John

APPLICANT: Mulero, Julio

TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE

TITLE OF INVENTION: POLYPEPTIDES

FILE REFERENCE: 28111/35908
CURRENT APPLICATION NUMBER: US/09/370,265
CURRENT FILING DATE: 1999-08-09
EARLIER APPLICATION NUMBER: PCT/US99/16180
EARLIER FILING DATE: 1999-07-16
EARLIER APPLICATION NUMBER: 09/350,836
EARLIER FILING DATE: 1999-07-09
EARLIER APPLICATION NUMBER: 09/273,447
EARLIER FILING DATE: 1999-03-19
EARLIER APPLICATION NUMBER: 09/244,444
EARLIER FILING DATE: 1999-02-04
EARLIER APPLICATION NUMBER: 09/122,449
EARLIER FILING DATE: 1998-07-24
EARLIER APPLICATION NUMBER: 09/118,205
EARLIER FILING DATE: 1998-07-16
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PatentIn Ver. 2.0
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LENGTH: 1287
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1284)
US-09-370-265-6

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Match	Length	DB	ID	Description
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2	1794.8	99.8	1799	13	US-10-091-085-2	Sequence 2, Appli
3	1794.8	99.8	1799	13	US-10-092-063-2	Sequence 2, Appli
4	1445	80.3	1601	12	US-10-286-926-24	Sequence 24, Appl
5	1445	80.3	1601	13	US-10-092-063-24	Sequence 24, Appl
6	1287	71.5	1287	12	US-10-286-926-4	Sequence 4, Appli
7	1287	71.5	1287	13	US-10-091-085-4	Sequence 4, Appli
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12	1089.2	60.5	1457	9	US-09-925-299-103	Sequence 103, App
13	1089.2	60.5	1457	11	US-09-925-299-103	Sequence 103, App
14	476	26.5	978	14	US-10-198-846-12729	Sequence 12729, A
15	359.2	20.0	420	10	US-09-960-352-11752	Sequence 11752, A
16	342.2	19.0	2693	12	US-10-286-926-48	Sequence 48, Appl

17	342.2	19.0	2762	12	US-10-286-926-26	Sequence 26, Appl
18	342.2	19.0	2762	12	US-10-286-926-52	Sequence 52, Appl
19	342.2	19.0	2762	13	US-10-092-063-26	Sequence 26, Appl
20	320.6	17.8	2371	12	US-10-286-926-46	Sequence 46, Appl
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22	320	17.8	342	10	US-09-998-598-1714	Sequence 1714, Ap
23	303.6	16.9	9365	12	US-10-286-926-8	Sequence 8, Appli
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40	145	8.1	461	9	US-09-864-761-723	Sequence 723, App
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42	141.8	7.9	239	9	US-09-864-761-17509	Sequence 17509, A
43	123.2	6.8	1900	12	US-10-286-926-47	Sequence 47, Appl
44	109.8	6.1	282	10	US-09-960-352-13474	Sequence 13474, A
45	106.8	5.9	587	13	US-10-027-632-12994	Sequence 12994, A

ALIGNMENTS

RESULT 1
US-10-286-926-2
; Sequence 2, Application US/10286926
; Publication No. US20030175752A1
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 28110/36457CON
; CURRENT APPLICATION NUMBER: US/10/286,926
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: 09/557,800
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/122449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/244444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1799
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS

LOCATION: (246)...(1529)
FEATURE:
NAME/KEY: misc feature
LOCATION: (1718)
OTHER INFORMATION: n = adenine or guanine or cytosine or thymidine
us-10-286-926-2

Query Match 99.8%; Score 1794.8; DB 12; Length 1799;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1799; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Publication No. US20020146772A1
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 28110/35761
; CURRENT APPLICATION NUMBER: US/10/091,085
; CURRENT FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09

PRIOR APPLICATION NUMBER: 09/273,447
PRIOR FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: 09/218,205
PRIOR FILING DATE: 1998-07-16
PRIOR APPLICATION NUMBER: 09/122,449
PRIOR FILING DATE: 1998-07-24
PRIOR APPLICATION NUMBER: 09/244,444
PRIOR FILING DATE: 1999-02-04
NUMBER OF SEQ ID NOS: 23

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 2

LENGTH: 1799

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (246)..(1529)

NAME/KEY: misc feature

LOCATION: (1718)

OTHER INFORMATION: n = adenine or guanine or cytosine or thymine

S-10-091-085-2

Query Match 99.8%; Score 1794.8; DB 13; Length 1799;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1799; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

y	1	GCGGGCTGCCGCGCAAGGTTGGCGCGCGCGCTTTTCCTGTTCCCTGGTCAACAAGAA	60
b	1	GCGGGCTGCCGCGCAAGGTTGGCGCGCGCGCTTTTCCTGTTCCCTGGTCAACAAGAA	60
y	61	TGTGGAGTGTCTTGGCTGAATCCTCATACAGACAAGATCATTTATGGTGTAGGTGA	120
b	61	TGTGGAGTGTCTTGGCTGAATCCTCATACAGACAAGATCATTTATGGTGTAGGTGA	120
y	121	AAAGTGATATATAAAGGACCAAGGAGAAATTCAGAAGGAAGAAAAATGGCTCT	180
b	121	AAAGTGATATATAAAGGACCAAGGAGAAATTCAGAAGGAAGAAAAATGGCTCT	180
y	181	GCAGGTGTGCGAGCAGGATTGCTTCTGCAACAAAGCTCCACCCAGCCACATCTTGGGA	240
b	181	GCAGGTGTGCGAGCAGGATTGCTTCTGCAACAAAGCTCCACCCAGCCACATCTTGGGA	240
y	241	AAAGATGGCCACTCTTGGGACACAGTCTTTTTCATGCTGGTGGTATCCTGTCTCCATGT	300
b	241	AAAGATGGCCACTCTTGGGACACAGTCTTTTTCATGCTGGTGGTATCCTGTCTCCATGT	300
y	301	GCGTGTCTCCACAGGAACCCAGCAGACTTGGTTTGAAGTATCTTCCGTCTCCATGT	360
b	301	GCGTGTCTCCACAGGAACCCAGCAGACTTGGTTTGAAGTATCTTCCGTCTCCATGT	360
y	361	GCCCATCAATGTGACGCGCCAGCCTTGTATGGAATATGTTTGTATGCGAGGAGCCTG	420
b	361	GCCCATCAATGTGACGCGCCAGCCTTGTATGGAATATGTTTGTATGCGAGGAGCCTG	420
y	421	GAACTCGAATTCATGTTTACACCTTTGTGCAGAAATGCCAGGACAGCTTCCAAATCTAG	480
b	421	GAACTCGAATTCATGTTTACACCTTTGTGCAGAAATGCCAGGACAGCTTCCAAATCTAG	480
y	481	AAGGGGAAGTCTTTGATTCGTGAAGCCAGGACTTTCTGCTTTTGTAGATCAACCTAAGC	540
b	481	AAGGGGAAGTCTTTGATTCGTGAAGCCAGGACTTTCTGCTTTTGTAGATCAACCTAAGC	540
y	541	AGGTGCTGAGACCGTTTCAAGGCTCTTAGAGGTGGCCAAAGACTCAATCCCGGAAGTC	600
b	541	AGGTGCTGAGACCGTTTCAAGGCTCTTAGAGGTGGCCAAAGACTCAATCCCGGAAGTC	600
y	601	ACTGGAAGAGACCCCGAGTGTCTTAAAGGCAACAGCAGGACTACGCTTACTGCCAGAAC	660
b	601	ACTGGAAGAGACCCCGAGTGTCTTAAAGGCAACAGCAGGACTACGCTTACTGCCAGAAC	660
y	661	ACAAAGCCAGGCTCTGCTCTTTGAGGTTAAAGGAGATCTTCAGGAAGTCACTTCTCTGG	720
b	661	ACAAAGCCAGGCTCTGCTCTTTGAGGTTAAAGGAGATCTTCAGGAAGTCACTTCTCTGG	720

QY	721	TACCAAGGGCAGTGTTAGCATCATGGATGGATCCGACGAAGGCATATTAGCTTGGGTTA	780
Db	721	TACCAAGGGCAGTGTTAGCATCATGGATGGATCCGACGAAGGCATATTAGCTTGGGTTA	780
QY	781	CTGTGAATTTTCTGACAGGTGAGTGCATGGCCACAGACAGAGACTGTGGGGACCTTGG	840
Db	781	CTGTGAATTTTCTGACAGGTGAGTGCATGGCCACAGACAGAGACTGTGGGGACCTTGG	840
QY	841	ACCTAGGGGAGCCTCCACCCAAATCACGTTCTCTGCCCCAGTTTGAGAAAACCTCTGGAAC	900
Db	841	ACCTAGGGGAGCCTCCACCCAAATCACGTTCTCTGCCCCAGTTTGAGAAAACCTCTGGAAC	900
QY	901	AAACTCCTAGGGGTACCTCACTTCCTTTGAGATGTTTAAACAGCACTTATAAGCTCTATA	960
Db	901	AAACTCCTAGGGGTACCTCACTTCCTTTGAGATGTTTAAACAGCACTTATAAGCTCTATA	960
QY	961	CACATAGTTACCTGGGATTGGAATTGAAAGCTGCAAGACTAGCAACCTTGGGAGCCCTGG	1020
Db	961	CACATAGTTACCTGGGATTGGAATTGAAAGCTGCAAGACTAGCAACCTTGGGAGCCCTGG	1020
QY	1021	AGACAGAGGGACTGATGGGCACACTTTCCGGAGTGCCCTGTTTACCGAGATGTTTGGAG	1080
Db	1021	AGACAGAGGGACTGATGGGCACACTTTCCGGAGTGCCCTGTTTACCGAGATGTTTGGAG	1080
QY	1081	CAGAGTGGATCTTTGGGGGTGTGAATACCAAGTATGGTGGCAACCAAGAGGGAGGTGG	1140
Db	1081	CAGAGTGGATCTTTGGGGGTGTGAATACCAAGTATGGTGGCAACCAAGAGGGAGGTGG	1140
QY	1141	GCTTTGAGCCCTGCTATGCCGAAGTCTGAGGGTGGTACGAGAAAACCTTACCCAGCCAG	1200
Db	1141	GCTTTGAGCCCTGCTATGCCGAAGTCTGAGGGTGGTACGAGAAAACCTTACCCAGCCAG	1200
QY	1201	AGGAGTCCAGAGAGGTTCCTTCTATGCTTTCTTACTATTATGACCGAGCTGTTGACA	1260
Db	1201	AGGAGTCCAGAGAGGTTCCTTCTATGCTTTCTTACTATTATGACCGAGCTGTTGACA	1260
QY	1261	CAGACATGATTGATTGAAAAGGGGGTATTTTAAAGTTGAAGATTTTGAAGAAAAG	1320
Db	1261	CAGACATGATTGATTGAAAAGGGGGTATTTTAAAGTTGAAGATTTTGAAGAAAAG	1320
QY	1321	CCAGGGAGTGTGTGATAACTTGGAAAACCTTCACTCAGGCGAGTCTTCTCTGTCATGG	1380
Db	1321	CCAGGGAGTGTGTGATAACTTGGAAAACCTTCACTCAGGCGAGTCTTCTCTGTCATGG	1380
QY	1381	ATCTCAGCTACATCACAGCCCTGTTAAAGGATGGCTTTGGCTTGCAGACAGCACAGTCT	1440
Db	1381	ATCTCAGCTACATCACAGCCCTGTTAAAGGATGGCTTTGGCTTGCAGACAGCACAGTCT	1440
QY	1441	TACAGCTCAAAAGAAAGTGAACAACATAGAGACGGGCTGGGCTTGGGGCCACCTTTC	1500
Db	1441	TACAGCTCAAAAGAAAGTGAACAACATAGAGACGGGCTGGGCTTGGGGCCACCTTTC	1500
QY	1501	ACCTGTTGCAGTCTCTGGGCACTCTCCATTGAGGCCACGTACTCTTGGAGACCTGCA	1560
Db	1501	ACCTGTTGCAGTCTCTGGGCACTCTCCATTGAGGCCACGTACTCTTGGAGACCTGCA	1560
QY	1561	TTGCCAACACCTTTTAAAGGGGAGGAGAGACACTTAGTTTCTGAACCTAGTCTGGGGACA	1620
Db	1561	TTGCCAACACCTTTTAAAGGGGAGGAGAGACACTTAGTTTCTGAACCTAGTCTGGGGACA	1620
QY	1621	TCCTGGACTGAGCCTAGAGATTWRGTTAATTAASCGGCCGAGCTTATCCTTWTATRAGGT	1680
Db	1621	TCCTGGACTGAGCCTAGAGATTWRGTTAATTAASCGGCCGAGCTTATCCTTWTATRAGGT	1680
QY	1681	AATTTACTTGCMTGGCCGCTTTACACGTCTGTATGNNAAACCTGCGTCCCAACTAACGC	1740
Db	1681	AATTTACTTGCMTGGCCGCTTTACACGTCTGTATGNNAAACCTGCGTCCCAACTAACGC	1740
QY	1741	TTGASAMATCCCCTTCGCAGCTGCGATACCAAAAGCCGACGACGCTTCCACAGTGCCA	1799
Db	1741	TTGASAMATCCCCTTCGCAGCTGCGATACCAAAAGCCGACGACGCTTCCACAGTGCCA	1799

RESULT 3
US-10-092-063-2
Sequence 2, Application US:10092063
Publication No. US2002017305A1
GENERAL INFORMATION:
APPLICANT: Ford, John
APPLICANT: Mulero, Julio
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE POLYPEPTIDES
FILE REFERENCE: 28110/35908
CURRENT APPLICATION NUMBER: US/10/092,063
CURRENT FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: 09/370,265
PRIOR FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: PCT/US99/16180
PRIOR FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: 09/350,836
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 09/273,447
PRIOR FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: 09/244,444
PRIOR FILING DATE: 1999-02-04
PRIOR APPLICATION NUMBER: 09/122,449
PRIOR FILING DATE: 1998-07-24
PRIOR APPLICATION NUMBER: 09/18,205
PRIOR FILING DATE: 1998-07-16
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 2
LENGTH: 1799
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (246)..(1529)
NAME/KEY: misc_feature
LOCATION: (1718)
OTHER INFORMATION: n = adenine or guanine or cytosine or thymine
S-10-092-063-2
Query Match 99.8%; Score 1794.8; DB 13; Length 1799;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1799; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
y 1 GCGGGCTGCCGCAAGGGTGGCGCGCGGGTTCCTTGTTCCTGGTCAACAAAGAAA 60
b 1 GCGGGCTGCCGCAAGGGTGGCGCGCGGGTTCCTTGTTCCTGGTCAACAAAGAAA 60
y 61 TGTGGAGTGTCTGGCTGAATCCTCATACAGACAAGATCATATGCTGCTTAGCTTGA 120
b 61 TGTGGAGTGTCTGGCTGAATCCTCATACAGACAAGATCATATGCTGCTTAGCTTGA 120
y 121 AAAAGTGATATAATAAAGGAACCAAGGAGAAATTCAGAGGAGAAAGAAATTCCTCT 180
b 121 AAAAGTGATATAATAAAGGAACCAAGGAGAAATTCAGAGGAGAAAGAAATTCCTCT 180
y 181 GCAGGTGTGGAGCAGGATTGCTTCTGCAACAAAGCCTCCACCCAGCCACATCTGGGA 240
b 181 GCAGGTGTGGAGCAGGATTGCTTCTGCAACAAAGCCTCCACCCAGCCACATCTGGGA 240
y 241 AAAGAATGGCCACTCTTGGGACACAGTCTTTTTCATGCTGTGGTATCCTGTGTTGCA 300
b 241 AAAGAATGGCCACTCTTGGGACACAGTCTTTTTCATGCTGTGGTATCCTGTGTTGCA 300
y 301 GCGCTGTCTCCACAGGAACCCAGCAGACTTGGTTTGAAGGTAATCTTCTCTTCATGT 360
b 301 GCGCTGTCTCCACAGGAACCCAGCAGACTTGGTTTGAAGGTAATCTTCTCTTCATGT 360
y 361 GCCCCATCAATGTACGCGCCAGCACCTTGTATGGAATATGTTTATGTCAGGGAGACTG 420
b 361 GCCCCATCAATGTACGCGCCAGCACCTTGTATGGAATATGTTTATGTCAGGGAGACTG 420
y 421 GAACTCGAATTCATGTTTACACCTTTGTGCAGAAATGCCAGSACAGCTTCCAAATCTAG 480

Db 421 GAACTCGAATTCATGTTTACACCTTTGTGCAGAAATGCCAGSACAGCTTCCAAATCTAG 480
Qy 481 AAGGGGAAGTTTTTGAATCTGTGAAGCCAGGACTTTCTGCTTTTGTAGATCAACCTAAGC 540
Db 481 AAGGGGAAGTTTTTGAATCTGTGAAGCCAGGACTTTCTGCTTTTGTAGATCAACCTAAGC 540
Qy 541 AGGGTGTCTGAGACCGTTCAAGGGCTCTTAGAGGTGGCCAAAGACTCAATCCCCGAAGTC 600
Db 541 AGGGTGTCTGAGACCGTTCAAGGGCTCTTAGAGGTGGCCAAAGACTCAATCCCCGAAGTC 600
Qy 601 ACTGGAAGAACCCAGTGTCTTAAAGGCAACAGCAGGACTACGGTTACTGCCAGAAC 660
Db 601 ACTGGAAGAACCCAGTGTCTTAAAGGCAACAGCAGGACTACGGTTACTGCCAGAAC 660
Qy 661 ACAAAGCCAAAGGCTCTGCTCTTTGAGGTAAGGAGATCTTCAGGAAGTCACCTTTCCTGG 720
Db 661 ACAAAGCCAAAGGCTCTGCTCTTTGAGGTAAGGAGATCTTCAGGAAGTCACCTTTCCTGG 720
Qy 721 TACCAAGGGCAGTGTAGCATCATGATGGATCCGACGAGGATATAGCTTGGGTTA 780
Db 721 TACCAAGGGCAGTGTAGCATCATGATGGATCCGACGAGGATATAGCTTGGGTTA 780
Qy 781 CTGTGAATTTTCTGACAGGTCAGCTGCATGSCCAGACAGAGACTGTGGGACCTTGG 840
Db 781 CTGTGAATTTTCTGACAGGTCAGCTGCATGSCCAGACAGAGACTGTGGGACCTTGG 840
Qy 841 ACCTAGGGGAGCCTCCACCCAAATCACGTTCTGCTGCCCCAGTTTGAGAAACTCTGGAAC 900
Db 841 ACCTAGGGGAGCCTCCACCCAAATCACGTTCTGCTGCCCCAGTTTGAGAAACTCTGGAAC 900
Qy 901 AAACTCCTAGGGGTACCTCACTTCTTTGAGATGTTTAAACAGCACTTATAAGCTCTATA 960
Db 901 AAACTCCTAGGGGTACCTCACTTCTTTGAGATGTTTAAACAGCACTTATAAGCTCTATA 960
Qy 961 CACATAGTTACCTGGGATTTGGATTGAAAGCTGCAAGACTAGCAACCTTGGAGCCCTGG 1020
Db 961 CACATAGTTACCTGGGATTTGGATTGAAAGCTGCAAGACTAGCAACCTTGGAGCCCTGG 1020
Qy 1021 AGACAGAAGGGACTGATGGSCACACTTTCCGGAGTGCCTGTTTACCAGAGATGGTTGGAAG 1080
Db 1021 AGACAGAAGGGACTGATGGSCACACTTTCCGGAGTGCCTGTTTACCAGAGATGGTTGGAAG 1080
Qy 1081 CAGAGTGGATCTTTGGGGTGTGAAATACCAGTATGTTGGCAACCAAGAGGGGAGGTGG 1140
Db 1081 CAGAGTGGATCTTTGGGGTGTGAAATACCAGTATGTTGGCAACCAAGAGGGGAGGTGG 1140
Qy 1141 GCTTTAGCCCTGCTATGCCGAAGTGTCTGAGGTGGTACGAGGAAACTTCAACAGCCAG 1200
Db 1141 GCTTTAGCCCTGCTATGCCGAAGTGTCTGAGGTGGTACGAGGAAACTTCAACAGCCAG 1200
Qy 1201 AGGAGTCCAGAGAGTTCTTCTATGCTTTCTCTTACTATTATGACCGAGCTGTTGACA 1260
Db 1201 AGGAGTCCAGAGAGTTCTTCTATGCTTTCTCTTACTATTATGACCGAGCTGTTGACA 1260
Qy 1261 CAGACATGATTGATTATGAAAGGGGGGTATTTTAAAGTTGAAGATTTGAAAGAAAAG 1320
Db 1261 CAGACATGATTGATTATGAAAGGGGGGTATTTTAAAGTTGAAGATTTGAAAGAAAAG 1320
Qy 1321 CCAGGGAAGTGTGTATAACTTGGAAACTTCACCTCAGGCAGTCTTCTGTCATGG 1380
Db 1321 CCAGGGAAGTGTGTATAACTTGGAAACTTCACCTCAGGCAGTCTTCTGTCATGG 1380
Qy 1381 ATCTCAGCTACATCAGACCCCTGTTTAAAGGATGGCTTTGGCTTTGCAGACAGCAGTCT 1440
Db 1381 ATCTCAGCTACATCAGACCCCTGTTTAAAGGATGGCTTTGGCTTTGCAGACAGCAGTCT 1440
Qy 1441 TACAGCTCACAAAGAAAGTGAACAACATAGACGGGCTGGCCCTTGGGGCCACCTTTC 1500
Db 1441 TACAGCTCACAAAGAAAGTGAACAACATAGACGGGCTGGCCCTTGGGGCCACCTTTC 1500
Qy 1501 ACCTGTTGAGTCTCTGGGCATCTCCCATTTGAGGCCACGTAATTCCTTGGAGACCTGCAT 1560
Db 1501 ACCTGTTGAGTCTCTGGGCATCTCCCATTTGAGGCCACGTAATTCCTTGGAGACCTGCAT 1560

b 1501 AACTGTTGCAGTCTCTGGGCACTCTCCCAATTGAGGCCACGTACTTCCTTGGAGACCTGCAAT 1560
y 1561 TTGCCAACACCTTTTAAAGGGAGGAGAGACACTTACTTCTGAACTAGTCTGGGGACA 1620
D 1561 TTGCCAACACCTTTTAAAGGGAGGAGAGACACTTACTTCTGAACTAGTCTGGGGACA 1620
y 1621 TCCTGGACTTGAGCCTTAGAGATTWRGTTAATTAAASCGCCGAGCTTATCCTTWATRAGGT 1680
D 1621 TCCTGGACTTGAGCCTTAGAGATTWRGTTAATTAAASCGCCGAGCTTATCCTTWATRAGGT 1680
y 1681 AATTACTTGCMTGGCCCGGTTTACACGTCGTGATGGNAACCTTCCGTCCTTAAACGC 1740
b 1681 AATTACTTGCMTGGCCCGGTTTACACGTCGTGATGGNAACCTTCCGTCCTTAAACGC 1740
y 1741 TTGASAMATCCCCCTTCGCAGCTGCGATACCAAAAGCCGACGCGCTTCCACAGTGCCA 1799
b 1741 TTGASAMATCCCCCTTCGCAGCTGCGATACCAAAAGCCGACGCGCTTCCACAGTGCCA 1799

ESULT 4

S-10-286-926-24

Sequence 24, Application US/10286926

Publication No. US20030175752A1

GENERAL INFORMATION:

APPLICANT: Ford, John

APPLICANT: Mulero, Julio

APPLICANT: Yeung, George

TITLE OF INVENTION: Methods and Materials Relating to CD39-Like

TITLE OF INVENTION: Polypeptides

FILE REFERENCE: 28110/36457CCN

CURRENT APPLICATION NUMBER: US/10/286,926

CURRENT FILING DATE: 2002-11-01

PRIOR APPLICATION NUMBER: 09/557,800

PRIOR FILING DATE: 2000-04-25

PRIOR APPLICATION NUMBER: 09/481,238

PRIOR FILING DATE: 2000-01-11

PRIOR APPLICATION NUMBER: 09/370,265

PRIOR FILING DATE: 1999-08-09

PRIOR APPLICATION NUMBER: PCT/US99/16180

PRIOR FILING DATE: 1999-07-16

PRIOR APPLICATION NUMBER: 09/350836

PRIOR FILING DATE: 1999-07-09

PRIOR APPLICATION NUMBER: 09/273447

PRIOR FILING DATE: 1999-03-19

PRIOR APPLICATION NUMBER: 09/122449

PRIOR FILING DATE: 1998-07-24

PRIOR APPLICATION NUMBER: 09/244444

PRIOR FILING DATE: 1999-02-04

PRIOR APPLICATION NUMBER: 09/118,205

PRIOR FILING DATE: 1998-07-16

NUMBER OF SEQ ID NOS: 54

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 24

LENGTH: 1601

TYPE: DNA

ORGANISM: Homo sapiens

S-10-286-926-24

Query Match 80.3%; Score 1445; DB 12; Length 1601;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

/ 1 GCGGGTCCGCGCAAGGGTGGCGCGCGCGGTTTCTTCTGGTCAACAAAGAAA 60

D 1 GCGGGTCCGCGCAAGGGTGGCGCGCGCGGTTTCTTCTGGTCAACAAAGAAA 60

/ 61 TGTGAGTGTCTTGGCTGAATCCTCATAACAGACAGATCATTATGGTGTAGGTTGA 120

D 61 TGTGAGTGTCTTGGCTGAATCCTCATAACAGACAGATCATTATGGTGTAGGTTGA 120

/ 121 AAAAGTGATATAATAAGGAACCAAGGAGAAAATTCAGAGGAAAGAAAATTCCTCT 180

D 121 AAAAGTGATATAATAAGGAACCAAGGAGAAAATTCAGAGGAAAGAAAATTCCTCT 180

QY 181 GCAGGTGTGCGAGCAGGATTGCTTCTTGCAACAAAAGCCTCCACCCAGCCACATCTTTGGGA 240
Db 181 GCAGGTGTGCGAGCAGGATTGCTTCTTGCAACAAAAGCCTCCACCCAGCCACATCTTTGGGA 240
QY 241 AAAGAATGGCCACTTCTTGGGGCACAGTCTTTTTCATGCTGGTATCCTGTGTGCA 300
Db 241 AAAGAATGGCCACTTCTTGGGGCACAGTCTTTTTCATGCTGGTATCCTGTGTGCA 300
QY 301 GCGCTGTCTCCACAGGAACCCAGACACTTGGTTTGAGGGTATCTTCCGTCTTCCATGT 360
Db 301 GCGCTGTCTCCACAGGAACCCAGACACTTGGTTTGAGGGTATCTTCCGTCTTCCATGT 360
QY 361 GCGCCATCAATGTGAGCGCCAGCACCTTGTATCGAATATGTTTGATGCGAGGAGCACTG 420
Db 361 GCGCCATCAATGTGAGCGCCAGCACCTTGTATCGAATATGTTTGATGCGAGGAGCACTG 420
QY 421 GAACTCGAATTTCATGTTTACACCTTTGTGCGAAGAAATGCCAGGACAGCTTCCAATTCTAG 480
Db 421 GAACTCGAATTTCATGTTTACACCTTTGTGCGAAGAAATGCCAGGACAGCTTCCAATTCTAG 480
QY 481 AAGGGGAAGTTTTTGTGTTGTAAGCCAGGACTTTTCTGCTTTTGTAGATCAACCTAAGC 540
Db 481 AAGGGGAAGTTTTTGTGTTGTAAGCCAGGACTTTTCTGCTTTTGTAGATCAACCTAAGC 540
QY 541 AGGGTGTGAGACCGTTCAAGGGGCTCTTAGAGGTGGCCAAAAGACTCAATCCCCCGAAGTC 600
Db 541 AGGGTGTGAGACCGTTCAAGGGGCTCTTAGAGGTGGCCAAAAGACTCAATCCCCCGAAGTC 600
QY 601 ACTGGAAAAAGACCCCACTGGTCTTAAGGGCAACAGCAGGACTACGCTTACTGCCAGAAC 660
Db 601 ACTGGAAAAAGACCCCACTGGTCTTAAGGGCAACAGCAGGACTACGCTTACTGCCAGAAC 660
QY 661 ACAAGCCAAAGGCTCTGCTCTTTGAGGTAAAGGAGATCTTCAGGAAGTCACTTTCCTGG 720
Db 661 ACAAGCCAAAGGCTCTGCTCTTTGAGGTAAAGGAGATCTTCAGGAAGTCACTTTCCTGG 720
QY 721 TACCAAGGGCAGTGTAGCATCATGATGGATCCGACGAAGGCATATTAGCTTGGGTTA 780
Db 721 TACCAAGGGCAGTGTAGCATCATGATGGATCCGACGAAGGCATATTAGCTTGGGTTA 780
QY 781 CTGTGAATTTTCTGACAGTCAAGTGCATGSCCATGACAGACAGGAGACTGTGGGACCTTGG 840
Db 781 CTGTGAATTTTCTGACAGTCAAGTGCATGSCCATGACAGACAGGAGACTGTGGGACCTTGG 840
QY 841 ACCTAGGGGGAGCCTCCACCCAAATCACGTTCTTCCGCGGAGTGTGAGAAAATCTTGAAC 900
Db 841 ACCTAGGGGGAGCCTCCACCCAAATCACGTTCTTCCGCGGAGTGTGAGAAAATCTTGAAC 900
QY 901 AAACCTCCTAGGGGCTACCTCCTTCTTGTGATGTTTAAACAGCACTTATAGCTCTATA 960
Db 901 AAACCTCCTAGGGGCTACCTCCTTCTTGTGATGTTTAAACAGCACTTATAGCTCTATA 960
QY 961 CACATAGTTACCTGGGATTGGATTGAAAGCTGCAGACTAGCAACCTTGGGAGCCCTGG 1020
Db 961 CACATAGTTACCTGGGATTGGATTGAAAGCTGCAGACTAGCAACCTTGGGAGCCCTGG 1020
QY 1021 AGACAGAAGGGACTGATGGSCACACTTTCGCGAGTGCCTGTTTACCGAGATGGTTGGAAG 1080
Db 1021 AGACAGAAGGGACTGATGGSCACACTTTCGCGAGTGCCTGTTTACCGAGATGGTTGGAAG 1080
QY 1081 CAGAGTGGATCTTGGGGGTGTGAATACCAGTATGGTGGCAACCAAGAGGGGAGGTGG 1140
Db 1081 CAGAGTGGATCTTGGGGGTGTGAATACCAGTATGGTGGCAACCAAGAGGGGAGGTGG 1140
QY 1141 GCTTTGAGCCCTGCTATGCCGAAGTGTGAGGGTGGTACGAGGAAACCTTCACCAGCCAG 1200
Db 1141 GCTTTGAGCCCTGCTATGCCGAAGTGTGAGGGTGGTACGAGGAAACCTTCACCAGCCAG 1200
QY 1201 AGGAGGTCCAGAGAGGTTCTTCTATGCTTTCTTACTATTATGACCGAGCTTTGACA 1260
Db 1201 AGGAGGTCCAGAGAGGTTCTTCTATGCTTTCTTACTATTATGACCGAGCTTTGACA 1260


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Y 1261 CAGACATGATTGATTATGAAGAAGGGGGTATTTTAAAGTTGAAGATTTTGAAGAAAAG 1320
b 1261 CAGACATGATTGATTATGAAGAAGGGGGTATTTTAAAGTTGAAGATTTTGAAGAAAAG 1320
Y 1321 CCAGGGAAGTGTGTGATAACTTGGAAAACCTTCACTCAGGCAGTCCTTTCTGTGCATGG 1380
b 1321 CCAGGGAAGTGTGTGATAACTTGGAAAACCTTCACTCAGGCAGTCCTTTCTGTGCATGG 1380
Y 1381 ATCTCAGCTACATCACAGCCCTGTTAAAGGATGGCTTTGGCTTTGCAGACAGCACAGTCT 1440
b 1381 ATCTCAGCTACATCACAGCCCTGTTAAAGGATGGCTTTGGCTTTGCAGACAGCACAGTCT 1440
Y 1441 TACAG 1445
b 1441 TACAG 1445

RESULT 5
S-10-092-063-24
Sequence 24, Application US/20092063
Publication No. US20020173005A1
GENERAL INFORMATION:
APPLICANT: Ford, John
APPLICANT: Mulero, Julio
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD33-LIKE POLYPEPTIDES
FILE REFERENCE: 28110/35908
CURRENT APPLICATION NUMBER: US/10/092,063
CURRENT FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: 09/370,265
PRIOR FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: PCT/US99/16180
PRIOR FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: 09/350,836
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 09/273,447
PRIOR FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: 09/244,444
PRIOR FILING DATE: 1999-02-04
PRIOR APPLICATION NUMBER: 09/122,449
PRIOR FILING DATE: 1998-07-24
PRIOR APPLICATION NUMBER: 09/118,205
PRIOR FILING DATE: 1998-07-16
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 24
LENGTH: 1601
TYPE: DNA
ORGANISM: Homo sapiens
S-10-092-063-24

Query Match 80.3%; Score 1445; DB 13; Length 1601;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GCGGGCTGCCGCGCAAGGGTGGCGCGCGCGGTTTTCCTTGTTCCTGGTCAACAAAGAAA 60
1 GCGGGCTGCCGCGCAAGGGTGGCGCGCGGTTTTCCTTGTTCCTGGTCAACAAAGAAA 60

61 TGTGGAGTGTCTTGGCTGAATCCTCATACAGACAGATCATTATGTTGCTGTAGTTGA 120
61 TGTGGAGTGTCTTGGCTGAATCCTCATACAGACAGATCATTATGTTGCTGTAGTTGA 120

121 AAAAGTGATATAATAAAGGAACCAAGGAGAAAATTCAGAAAGGAAGAAAATTCCTCT 180
121 AAAAGTGATATAATAAAGGAACCAAGGAGAAAATTCAGAAAGGAAGAAAATTCCTCT 180

181 GCAGTGTGCGAGCAGGATTGCTTCTGCAACAAAAGCTCCACCCAGCCACATCTTGGGA 240
181 GCAGTGTGCGAGCAGGATTGCTTCTGCAACAAAAGCTCCACCCAGCCACATCTTGGGA 240

241 AAAGAAATGGCCACTTCITGGGGCACAGTCTTTTTCATGCTGGTGGTATCCTGTGTGCA 300
241 AAAGAAATGGCCACTTCITGGGGCACAGTCTTTTTCATGCTGGTGGTATCCTGTGTGCA 300
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QY 301 GCGTGTCTCCACAGGAACCAAGCAGACACTTGGTTTGAGGGTATCTTCCCTGTCTTCCATGT 360
Db 301 GCGTGTCTCCACAGGAACCAAGCAGACACTTGGTTTGAGGGTATCTTCCCTGTCTTCCATGT 360
QY 361 GCGCCATCAATGTCAGCCCGCAGCACCTTGTATGGAATATTATGTTGATGCGGGAGCACTG 420
Db 361 GCGCCATCAATGTCAGCCCGCAGCACCTTGTATGGAATATTATGTTGATGCGGGAGCACTG 420
QY 421 GAACTCGAATTTCATGTTTACACCTTTGTGAAGCCAGGACTTCTGCTTTTGTAGATCAACCTAAGC 540
Db 421 GAACTCGAATTTCATGTTTACACCTTTGTGAAGCCAGGACTTCTGCTTTTGTAGATCAACCTAAGC 540
QY 481 AAGGGGAAGTTTTTGTATCTGTGAAGCCAGGACTTCTGCTTTTGTAGATCAACCTAAGC 540
Db 481 AAGGGGAAGTTTTTGTATCTGTGAAGCCAGGACTTCTGCTTTTGTAGATCAACCTAAGC 540
QY 541 AGGGTGTGAGACCGTTCAAGGGCTCTTAGAGTGGGCCAAAAGACTCAATCCCCCGAAGTC 600
Db 541 AGGGTGTGAGACCGTTCAAGGGCTCTTAGAGTGGGCCAAAAGACTCAATCCCCCGAAGTC 600
QY 601 ACTGAAAAAGACCCCGAGTGTCTTAAAGGCAACAGCAGGACTACGCTTACTGCCAGAAC 660
Db 601 ACTGAAAAAGACCCCGAGTGTCTTAAAGGCAACAGCAGGACTACGCTTACTGCCAGAAC 660
QY 661 ACAAAAGCAAGGCTCTGCTCTTTGAGGTAAAGAGATCTTCAGGAAGTCACCTTCTCTGG 720
Db 661 ACAAAAGCAAGGCTCTGCTCTTTGAGGTAAAGAGATCTTCAGGAAGTCACCTTCTCTGG 720
QY 721 TACCAAAGGGCAGTGTTAGCATCATGGATGGATCCGACAGACAGGAGACTGCGGGACCTTGG 840
Db 721 TACCAAAGGGCAGTGTTAGCATCATGGATGGATCCGACAGGAGACTGCGGGACCTTGG 840
QY 781 CTGTGAATTTTCTGACAGGTCAGCTGCATGGCGCACAGACAGGAGACTGCGGGACCTTGG 840
Db 781 CTGTGAATTTTCTGACAGGTCAGCTGCATGGCGCACAGGAGACTGCGGGACCTTGG 840
QY 841 ACCTAGGGGGAGCCTCCACCCAAATCACGTTCTCTGCCCCCAGTTTGAAGAAACTCTGGAAC 900
Db 841 ACCTAGGGGGAGCCTCCACCCAAATCACGTTCTCTGCCCCCAGTTTGAAGAAACTCTGGAAC 900
QY 901 AAACCTCTAGGGGTACCTCACTTCTCTTTGAGATGTTTAAACAGCACTTATAAGCTCTATA 960
Db 901 AAACCTCTAGGGGTACCTCACTTCTCTTTGAGATGTTTAAACAGCACTTATAAGCTCTATA 960
QY 961 CACATAGTTACCTGGGATTTGGATTGAAAGCTGCAAGACTAGCAACCCCTGGGAGCCCTGG 1020
Db 961 CACATAGTTACCTGGGATTTGGATTGAAAGCTGCAAGACTAGCAACCCCTGGGAGCCCTGG 1020
QY 1021 AGACAGAAGGGACTGATGGGCACACTTTCGCGAGTGCCTGTTTACCGAGATGGTTGGAAG 1080
Db 1021 AGACAGAAGGGACTGATGGGCACACTTTCGCGAGTGCCTGTTTACCGAGATGGTTGGAAG 1080
QY 1081 CAGAGTGGATCTTTGGGGGTGTGAAATACCAATACCAGTATGGTGGCAACCAAGAGGGGAGGTGG 1140
Db 1081 CAGAGTGGATCTTTGGGGGTGTGAAATACCAATACCAGTATGGTGGCAACCAAGAGGGGAGGTGG 1140
QY 1141 GCTTTGAGCCCTGCTATGCCGAAGTGTCTGAGGGTGGTACGAGGAAAACCTTCACCAGCCAG 1200
Db 1141 GCTTTGAGCCCTGCTATGCCGAAGTGTCTGAGGGTGGTACGAGGAAAACCTTCACCAGCCAG 1200
QY 1201 AGGAGGTCCAGAGAGGTTCCTTCTATGCTTCTTACTTACTTATGACCGAGCTGTTGACA 1260
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QY 1261 CAGACATGATTGATTATGAAGAGGGGGTATTTTAAAGTTTGAAGATTTTGAAGAAAAAG 1320
Db 1261 CAGACATGATTGATTATGAAGAGGGGGTATTTTAAAGTTTGAAGATTTTGAAGAAAAAG 1320
QY 1321 CCAGGGAAGTGTGTGATAAATTGGAAAACCTTCACCTCAGGCAGTCTTCTCTGTCATGG 1380
Db 1321 CCAGGGAAGTGTGTGATAAATTGGAAAACCTTCACCTCAGGCAGTCTTCTCTGTCATGG 1380
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1381 ATCTCAGCTACATCAGCCCTGTTAAAGGATGGCTTTGGCTTTGCGACAGCAGACAGTCT 1440
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1381 ATCTCAGCTACATCAGCCCTGTTAAAGGATGGCTTTGGCTTTGCGACAGCAGACAGTCT 1440
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1441 TACAG 1445
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1441 TACAG 1445

RESULT 6

S-10-286-926-4
Sequence 4, Application US/10286926
Publication No. US20030175752A1
GENERAL INFORMATION:
APPLICANT: Ford, John
APPLICANT: Mulero, Julio
APPLICANT: Yeung, George
TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 28110/36457CON
CURRENT APPLICATION NUMBER: US/10/286,926
CURRENT FILING DATE: 2002-11-01
PRIOR APPLICATION NUMBER: 09/557,800
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/481,238
PRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: 09/370,265
PRIOR FILING DATE: 1999-08-09
PRIOR APPLICATION NUMBER: PCT/US99/16180
PRIOR FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: 09/350836
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 09/273447
PRIOR FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: 09/122449
PRIOR FILING DATE: 1998-07-24
PRIOR APPLICATION NUMBER: 09/244444
PRIOR FILING DATE: 1999-02-04
PRIOR APPLICATION NUMBER: 09/118,205
PRIOR FILING DATE: 1998-07-16
NUMBER OF SEQ ID NOS: 54
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 1287
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1284)
S-10-286-926-4
Query Match 71.5%; Score 1287; DB 12; Length 1287;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1287; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
246 ATGGCCACTTCTTGGGGCACAGTCTTTTCATGCTGGTGGTATCCTGTGTTGCAGCGCT 305
1 ATGGCCACTTCTTGGGGCACAGTCTTTTCATGCTGGTGGTATCCTGTGTTGCAGCGCT 60
306 GTCTCCACAGGAACAGCAGACTTGGTTGAGGATATCTTCCCTGTCTTCCATGTGCCCC 365
61 GTCTCCACAGGAACAGCAGACTTGGTTGAGGATATCTTCCCTGTCTTCCATGTGCCCC 120
366 ATCAATGTCAGCGCCAGCAGCTTGTATGGAATATCTTTGATGCGGGAGCAGTGGAACT 425
121 ATCAATGTCAGCGCCAGCAGCTTGTATGGAATATCTTTGATGCGGGAGCAGTGGAACT 180
426 CGAATTTCATGTTTACACCTTTGTGCAGAAAATGCCAGGACAGCTTCCAAATCTAGAAGGG 485
181 CGAATTTCATGTTTACACCTTTGTGCAGAAAATGCCAGGACAGCTTCCAAATCTAGAAGGG 240
486 GAAAGTTTTTGATTCTGTGAAGCCAGGACTTTCTGCTTTTGTAGATCAACCTAAGCAGGGT 545
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Db 241 GAAAGTTTTTGATTCTGTGAAGCCAGGACTTTCTGCTTTTGTAGATCAACCTAAGCAGGGT 300
Qy 546 GGTGAGACCGTTCAAGGGCTCTTTAGAGGTGGCCAAAGACTCAATCCCCCGAAGTCACTGG 605
Db 301 GCTGAGACCGTTCAAGGGCTCTTTAGAGGTGGCCAAAGACTCAATCCCCCGAAGTCACTGG 360
Qy 606 AAAAAAGACCCCGAGTGGTCTTAAAGGCAACAGCAGGACTACGCTTACTGCCAGAACACAAA 665
Db 361 AAAAAAGACCCCGAGTGGTCTTAAAGGCAACAGCAGGACTACGCTTACTGCCAGAACACAAA 420
Qy 666 GCCAAGGCTCTGCTCTTTGAGGTAAAGGAGATCTTCAAGGAAGTCACCTTTCTGGTACCA 725
Db 421 GCCAAGGCTCTGCTCTTTGAGGTAAAGGAGATCTTCAAGGAAGTCACCTTTCTGGTACCA 480
Qy 726 AAGGGCAGTGTTAGCATCATGGATGCCGACGAGGACATATTAGCTTGGGTACTGTG 785
Db 481 AAGGGCAGTGTTAGCATCATGGATGCCGACGAGGACATATTAGCTTGGGTACTGTG 540
Qy 786 AATTTTCTGACAGGTGAGTGCATGGCCACAGACGAGAGACTGTGGGACCTTGGACCTA 845
Db 541 AATTTTCTGACAGGTGAGTGCATGGCCACAGACGAGGAGACTGTGGGACCTTGGACCTA 600
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Qy 906 CCTAGGGGCTACCTCACTTCTTTGAGATGTTTAAACAGCAGCTTATAAGCTTATACACAT 965
Db 661 CCTAGGGGCTACCTCACTTCTTTGAGATGTTTAAACAGCAGCTTATAAGCTTATACACAT 720
Qy 966 AGTTACCTGGGATTTGGATTGAAAGCTGCAAGACTAGCAACCCCTGGAGCCCTGGAGACA 1025
Db 721 AGTTACCTGGGATTTGGATTGAAAGCTGCAAGACTAGCAACCCCTGGAGCCCTGGAGACA 780
Qy 1026 GAAGGACTGATGGGACACATTTCCGGAGTGCCTGTTTACCGAGATGTTTGGAGAGAGAG 1085
Db 781 GAAGGACTGATGGGACACATTTCCGGAGTGCCTGTTTACCGAGATGTTTGGAGAGAGAG 840
Qy 1086 TGGATCTTTGGGGGTGTAATACCAATACCAATGTTGGCAACCAAGAGGGGAGGTGGGCTTT 1145
Db 841 TGGATCTTTGGGGGTGTAATACCAATACCAATGTTGGCAACCAAGAGGGGAGGTGGGCTTT 900
Qy 1146 GAGCCCTGCTATGCCGAAGTCTGAGGGTGTACGAGGAAAACCTTCAACAGCCAGAGGAG 1205
Db 901 GAGCCCTGCTATGCCGAAGTCTGAGGGTGTACGAGGAAAACCTTCAACAGCCAGAGGAG 960
Qy 1206 GTCCAGAGAGGTTCCCTTCTATGCTTTCTCTTACTATTATGACCGAGCTGTTACACAGAC 1265
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Qy 1266 ATGATTGATTATGAAAAGGGGGTATTTTAAAGTTGAAGATTTTGAAGAAAAGCCAGG 1325
Db 1021 ATGATTGATTATGAAAAGGGGGTATTTTAAAGTTGAAGATTTTGAAGAAAAGCCAGG 1080
Qy 1326 GAAGTGTGTGATAACTTGGAAAACCTTCACCTCAGCAGTCCCTTCCCTGTGCAATGGATCTC 1385
Db 1081 GAAGTGTGTGATAACTTGGAAAACCTTCACCTCAGCAGTCCCTTCCCTGTGCAATGGATCTC 1140
Qy 1386 AGCTACATCACAGCCCTGTTAAAGGATGGCTTTGGCTTTGCAGACAGCAGTCTTACAG 1445
Db 1141 AGCTACATCACAGCCCTGTTAAAGGATGGCTTTGGCTTTGCAGACAGCAGTCTTACAG 1200
Qy 1446 CTCACAAAGAAAGTGAACAACATAGACCGGGCTGGGCCCTTGGGGGCCACCTTTTACACCTG 1505
Db 1201 CTCACAAAGAAAGTGAACAACATAGACCGGGCTGGGCCCTTGGGGGCCACCTTTTACACCTG 1260
Qy 1506 TTGCAGTCTCTGGGCATCTCCCATTTGA 1532
Db 1261 TTGCAGTCTCTGGGCATCTCCCATTTGA 1287

Sequence 4, Application US/10091085
Publication No. US20020146772A1
GENERAL INFORMATION:

APPLICANT: Ford, John

APPLICANT: Mulero, Julio

TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE

TITLE OF INVENTION: POLYPEPTIDES

FILE REFERENCE: 28110/35761

CURRENT APPLICATION NUMBER: US/10/091,085

CURRENT FILING DATE: 2002-03-05

PRIOR APPLICATION NUMBER: 09/350,836

PRIOR FILING DATE: 1999-07-09

PRIOR APPLICATION NUMBER: 09/273,447

PRIOR FILING DATE: 1999-03-19

PRIOR APPLICATION NUMBER: 09/118,205

PRIOR FILING DATE: 1998-07-16

PRIOR APPLICATION NUMBER: 09/122,449

PRIOR FILING DATE: 1998-07-24

PRIOR APPLICATION NUMBER: 09/244,444

PRIOR FILING DATE: 1999-02-04

NUMBER OF SEQ ID NOS: 23

SOFTWARE: Patent-In Ver. 2.0

SEQ ID NO 4

LENGTH: 1287

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (1)..(1284)

S-10-091-085-4

Query Match 71.5%; Score 1287; DB 13; Length 1287;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1287; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 246 ATGGCCACTTCTTGGGGCACAGTCTTTTTCATGCTGGTGGTATCCTGTGTTGCGAGCGCT 305
|||||
D 1 ATGGCCACTTCTTGGGGCACAGTCTTTTTCATGCTGGTGGTATCCTGTGTTGCGAGCGCT 60
|||||

Y 306 GTCTCCACAGGAACCCAGCAGACTTGGTTGAGGGTATCTTCTGCTTCCATGTGCCCC 365
|||||

D 61 GTCTCCACAGGAACCCAGCAGACTTGGTTGAGGGTATCTTCTGCTTCCATGTGCCCC 120
|||||

Y 366 ATCAATGTCAGGCCAGCAGCCTTGTATGGAATTAATGTTGATGAGGAGCAGGAGCAGTGGAACT 425
|||||

D 121 ATCAATGTCAGGCCAGCAGCCTTGTATGGAATTAATGTTGATGAGGAGCAGGAGCAGTGGAACT 180
|||||

Y 426 CGAATTCATGTTTACACCTTTGTGCAGAAATGCCAGGACAGCTTCCAAATTCAGAAAGGG 485
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D 181 CGAATTCATGTTTACACCTTTGTGCAGAAATGCCAGGACAGCTTCCAAATTCAGAAAGGG 240
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Y 486 GAAGTTTGTGTTGAGCCAGGACTTCTGCTTTTGTAGATCAACCTTAAGCAGGGT 545
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D 241 GAAGTTTGTGTTGAGCCAGGACTTCTGCTTTTGTAGATCAACCTTAAGCAGGGT 300
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Y 546 GCTGAGACCGTTCAAGGGCTCTTAGAGTGCCCAAGACTCAATCCCCGGAAGTCACTGG 605
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D 301 GCTGAGACCGTTCAAGGGCTCTTAGAGTGCCCAAGACTCAATCCCCGGAAGTCACTGG 360
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Y 606 AAAAAGACCCCACTGGTCTTAAGGCAACAGCAGGACTAGCTTACTGCCAGAACACAA 665
|||||

D 361 AAAAAGACCCCACTGGTCTTAAGGCAACAGCAGGACTAGCTTACTGCCAGAACACAA 420
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Y 666 GCCAAGGCTCTGCTCTTTGAGGTAAGGAGATCTTCAGGAAGTCACTTCTCTGTACCA 725
|||||

D 421 GCCAAGGCTCTGCTCTTTGAGGTAAGGAGATCTTCAGGAAGTCACTTCTCTGTACCA 480
|||||

Y 726 AAGGGCAGTGTAGCATCATGGATGATCCGACGAAGGCATATTAGCTGGGTTACTGTG 785
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D 481 AAGGGCAGTGTAGCATCATGGATGATCCGACGAAGGCATATTAGCTGGGTTACTGTG 540
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Y 786 AATTTCTGACAGGTCAGCTGCATGGCCACAGACAGGAGACTGTGGGACCTTGGACCTA 845
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Db 541 AATTTCTGACAGGTGAGTGTGATGCGCCACAGACAGGAGACTGTGGGACCTTGGACCTA 600
Qy GGGGAGCCTCCACCCAAATCACGTTCTCTGCCCCAGTTTGAGAAAACTCTGGAACAACT 905
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Db 501 GGGGAGCCTCCACCCAAATCACGTTCTCTGCCCCAGTTTGAGAAAACTCTGGAACAACT 660
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Qy 906 CCTAGGGGCTACCTCACTTCTCTTTGAGATGTTTAAACAGCACTTATAAGCTCTATACAT 965
|||
Db 561 CCTAGGGGCTACCTCACTTCTCTTTGAGATGTTTAAACAGCACTTATAAGCTCTATACAT 720
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Qy 966 AGTTACCTGGGATTGGATTGAAAGCTGCAAGACTAGCAACCTTGGGAGCCCTGGAGACA 1025
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Db 721 AGTTACCTGGGATTGGATTGAAAGCTGCAAGACTAGCAACCTTGGGAGCCCTGGAGACA 780
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Qy 1026 GAAGGACTGATGGGCACACTTTCGGGAGTGCCTGTATTACCGAGATGGTTGGAGCAGAG 1085
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Db 781 GAAGGACTGATGGGCACACTTTCGGGAGTGCCTGTATTACCGAGATGGTTGGAGCAGAG 840
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Qy 1086 TGGATCTTTGGGGTGTGAAATACCACTATGGTGGCAACCAAGAGGGGAGGTGGGCTTT 1145
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Qy 1146 GAGCCCTGCTATGCCGAAGTGTCTGAGGGTGTACGAGGAAATTCACCCAGCCAGAGGAG 1205
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Qy 1326 GAAGTGTGTGATAACTTGGAAAACTTCACCTCAGGCACTTCTCTGTGCATGGATCTC 1385
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Db 1081 GAAGTGTGTGATAACTTGGAAAACTTCACCTCAGGCACTTCTCTGTGCATGGATCTC 1140
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Qy 1386 AGCTACATCACAGCCCTGTAAAGGATGGCTTTGGCTTTGCAGACAGCAGTCTTACAG 1445
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Db 1141 AGCTACATCACAGCCCTGTAAAGGATGGCTTTGGCTTTGCAGACAGCAGTCTTACAG 1200
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Qy 1446 CTCACAAAGAAAGTGAACAACATAGAGACGGCTGGGCTTGGGGCCACCTTTTCACCTG 1505
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Db 1201 CTCACAAAGAAAGTGAACAACATAGAGACGGCTGGGCTTGGGGCCACCTTTTCACCTG 1260
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Qy 1506 TTGCAGTCTCTGGGCATCTCCCATTTGA 1532
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Db 1261 TTGCAGTCTCTGGGCATCTCCCATTTGA 1287
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RESULT 8

US-10-092-063-4

; Sequence 4, Application US/10092063

; Publication No. US20020173005A1

; GENERAL INFORMATION:

; APPLICANT: Ford, John

; APPLICANT: Mulero, Julio

; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE POLYPEPTIDES

; FILE REFERENCE: 28110/35908

; CURRENT APPLICATION NUMBER: US/10/092,063

; CURRENT FILING DATE: 2002-03-05

; PRIOR APPLICATION NUMBER: 09/370,265

; PRIOR FILING DATE: 2002-01-31

; PRIOR APPLICATION NUMBER: PCT/US99/16180

; PRIOR FILING DATE: 1999-07-16

; PRIOR APPLICATION NUMBER: 09/350,836

; PRIOR FILING DATE: 1999-07-09

; PRIOR APPLICATION NUMBER: 09/273,447

; PRIOR FILING DATE: 1999-03-19

; PRIOR APPLICATION NUMBER: 09/244,444

; PRIOR FILING DATE: 1999-02-04

; PRIOR APPLICATION NUMBER: 09/122,449

PRIOR FILING DATE: 1998-07-24
PRIOR APPLICATION NUMBER: 09/118,205
PRIOR FILING DATE: 1998-07-16
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 1287
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1284)
S-10-092-063-4
Query Match 71.5%; Score 1287; DB 13; Length 1287;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1287; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Y 246 ATGGCCACTTCTTGGGGCACAGTCTTTTTCATGCTGGTGGTATCCTGTGTTGCAGCGCT 305
b 1 ATGGCCACTTCTTGGGGCACAGTCTTTTTCATGCTGGTGGTATCCTGTGTTGCAGCGCT 60
Y 306 GTCTCCACAGGAACCCAGCAGACTTGGTTTGAGGGTATCTTCTGTCTTCCATGTGCCCC 365
b 61 GTCTCCACAGGAACCCAGCAGACTTGGTTTGAGGGTATCTTCTGTCTTCCATGTGCCCC 120
Y 366 ATCAATGTGAGCGCCAGCAGCCTTGTATGGAATTATGTTGATGCGAGGAGCACTGGAAT 425
b 121 ATCAATGTGAGCGCCAGCAGCCTTGTATGGAATTATGTTGATGCGAGGAGCACTGGAAT 180
Y 426 CGAATTCTATGTTTACACCTTTGTGCAGAAAATGCCAGACAGCTTCCAAATCTAGAAGGG 485
b 181 CGAATTCTATGTTTACACCTTTGTGCAGAAAATGCCAGGACAGCTTCCAAATCTAGAAGGG 240
Y 486 GAAGTTTGTGATCTCTGTAAGCCAGGACTTTCTGCTTTGTAGATCAACCTTAAGCAGGGT 545
D 241 GAAGTTTGTGATCTCTGTAAGCCAGGACTTTCTGCTTTGTAGATCAACCTTAAGCAGGGT 300
Y 546 GCTGAGACCGTTCAGGGCTCTTAGAGGTGGCCAAAGACTCAATCCCGGAGTCACTGG 605
D 301 GCTGAGACCGTTCAGGGCTCTTAGAGGTGGCCAAAGACTCAATCCCGGAGTCACTGG 360
Y 606 AAAAAGACCCCAAGTCTCTTAAGGCAACAGCAGGACTAGCTTACTGCCAGAACACAAA 665
D 361 AAAAAGACCCCAAGTCTCTTAAGGCAACAGCAGGACTAGCTTACTGCCAGAACACAAA 420
Y 666 GCCAAGGCTCTGCTCTTTGAGGTAAAGGAGATCTTCAAGAACTCACTTTCTGGTACCA 725
D 421 GCCAAGGCTCTGCTCTTTGAGGTAAAGGAGATCTTCAAGAACTCACTTTCTGGTACCA 480
Y 726 AAGGGAGTGTAGCATCATGATGGAATCCGACGAAGCATATTAGCTTGGGTACTGTG 785
D 481 AAGGGAGTGTAGCATCATGATGGAATCCGACGAAGCATATTAGCTTGGGTACTGTG 540
Y 786 AATTTCTGACAGGTCAAGTCAATGCTGATGGCCACAGACAGGAGACTGTGGGACCTTGGACCTA 845
D 541 AATTTCTGACAGGTCAAGTCAATGCTGATGGCCACAGACAGGAGACTGTGGGACCTTGGACCTA 600
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D 601 GGGGAGGCTCCACCCAAATCAGTTCCTGCCCCAGTTTGAGAAAACCTCTGGAACAAACT 660
Y 906 CCTAGGGCTACCTCACTTCTTTGAGATGTTTAACAGCACTTATAAGCTCTATACACAT 965
D 661 CCTAGGGCTACCTCACTTCTTTGAGATGTTTAACAGCACTTATAAGCTCTATACACAT 720
Y 966 AGTTACCTGGGATTTGGATTGAAAGCTGCAAGACTAGCACCTTGGAGCCCTGGAGACA 1025
D 721 AGTTACCTGGGATTTGGATTGAAAGCTGCAAGACTAGCACCTTGGAGCCCTGGAGACA 780
Y 1026 GAAGGGACTGATGGGCACACTTTCCGGAGTGCCTGTTTACCGAGATGGTTGGAAGCAGAG 1085
D 781 GAAGGGACTGATGGGCACACTTTCCGGAGTGCCTGTTTACCGAGATGGTTGGAAGCAGAG 840

Y 1086 TGGATCTTTGGGGTGTGAAATACCAAGTATGGTGCACCAAGAAAGGGAGGTGGCTTT 1145
D 841 TGGATCTTTGGGGTGTGAAATACCAAGTATGGTGCACCAAGAAAGGGAGGTGGCTTT 900
Y 1146 GAGCCCTGCTATGCCAAGTGTCTGAGGGTGGTACGAGGAAAACCTTCAACAGCCAGAGGAG 1205
D 901 GAGCCCTGCTATGCCAAGTGTCTGAGGGTGGTACGAGGAAAACCTTCAACAGCCAGAGGAG 960
Y 1206 GTCCAGAGAGGTTCCCTTCTATGCTTTCTTACTATTATGACCGAGTGTGACACAGAC 1265
D 961 GTCCAGAGAGGTTCCCTTCTATGCTTTCTTACTATTATGACCGAGTGTGACACAGAC 1020
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D 1021 ATGATTGATTATGAAAAGGGGGTATTTTAAAGTGTGAAGATTTTGAAGAAGAAAGCCAGG 1080
Y 1326 GAAGTGTGTGATAACTTGGAAAACCTTCACCTCAGGCAGTCCCTTTCCTGTGCATGGATCTC 1385
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Y 1506 TTGCAGTCTCTGGGCATCTCCCATTTGA 1532
D 1261 TTGCAGTCTCTGGGCATCTCCCATTTGA 1287

RESULT 9
US-10-286-926-6
; Sequence 6, Application US/10286926
; Publication No. US20030175752A1
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 28110/36457CON
; CURRENT APPLICATION NUMBER: US/10/286,926
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: 09/557,800
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/122449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/244444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1287
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS

LOCATION: (1)..(1284)									
-10-286-926-6									
Query Match 71.0%; Score 1277.4; DB 12; Length 1287;									
Best Local Similarity 99.5%; Pred. No. 0;									
Matches 1281; Conservative 0; Mismatches 6; Indels 0; Gaps 0;									
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Qy	306	GTCTCCACAGGAACCCAGCAGACTTGGTTTGAGGGTATCTTCTGTCTTCCATGTGCCCC	365						
Db	61	GTCTCCACAGGAACCCAGCAGACTTGGTTTGAGGGTATCTTCTGTCTTCCATGTGCCCC	120						
Qy	366	ATCAATGTCAGCGCCAGCACCTTGTATGGAATATGTTTGTATGCAGGAGCACTGGAACT	425						
Db	121	ATCAATGTCAGCGCCAGCACCTTGTATGGAATATGTTTGTATGCAGGAGCACTGGAACT	180						
Qy	426	CGAATTCATGTTTACACCTTTGTGCAGAAAATGCCAGGACAGCTTCCAAATCTAGAGGG	485						
Db	181	CGAATTCATGTTTACACCTTTGTGCAGAAAATGCCAGGACAGCTTCCAAATCTAGAGGG	240						
Qy	486	GAAGTTTTTGTGTTGTAAGCCAGGACTTCTGCTTTTGTAGATCAACCTAAGCAGGGT	545						
Db	241	GAAGTTTTTGTGTTGTAAGCCAGGACTTCTGCTTTTGTAGATCAACCTAAGCAGGGT	300						
Qy	546	GCTGAGACCGTTCAAGGGCTCTTAGAGGTGGCCAAAGACTCAATCCCGGAAGTCACTGG	605						
Db	301	GCTGAGACCGTTCAAGGGCTCTTAGAGGTGGCCAAAGACTCAATCCCGGAAGTCACTGG	360						
Qy	606	AAAAAGACCCAGTGGTCTTAAGGCAACAGCAGGACTACGCTTACTGCCAGAACACAAA	665						
Db	361	AAAAAGACCCAGTGGTCTTAAGGCAACAGCAGGACTACGCTTACTGCCAGAACACAAA	420						
Qy	666	GCCAGGCTCTGCTCTTTGAGGTAAGGAGATCTTCCAGGAAGTCACTTCTCTGGTACCA	725						
Db	421	GCCAGGCTCTGCTCTTTGAGGTAAGGAGATCTTCCAGGAAGTCACTTCTCTGGTACCA	480						
Qy	726	AAGGGCAGTGTAGCATCATGATGGATCCGACGAGGCATATTAGCTTGGGTTACTGTG	785						
Db	481	AAGGGCAGTGTAGCATCATGACTGGACAGCAGGACATATTCGCTTGGGTTACTGTG	540						
Qy	786	AATTTTCTGACAGGTCAGCTGCATGGCCACAGACAGGAGACTGTGGGACCTTGGACCTA	845						
Db	541	AATTTTCTGACAGGTCAGCTGCATGGCCACAGACAGGAGACTGTGGGACCTTGGACCTA	600						
Qy	846	GGGGAGCCTCCACCCAAATCAGCTTCTGCCCCAGTTTGAGAAAACCTCTGGAACAAACT	905						
Db	601	GGGGAGCCTCCACCCAAATCAGCTTCTGCCCCAGTTTGAGAAAACCTCTGGAACAAACT	660						
Qy	906	CCTAGGGCTACCTCACTTCTCTTTGAGATGTTTACAGCACTTATAAGCTCTATACACAT	965						
Db	661	CCTAGGGCTACCTCACTTCTCTTTGAGATGTTTACAGCACTTATAAGCTCTATACACAT	720						
Qy	966	AGTTACTGGGATTTGATTGAAAGCTGCAAGACTAGCAACCTGGGAGCCCTGGAGACA	1025						
Db	721	AGTTACTGGGATTTGATTGAAAGCTGCAAGACTAGCAACCTGGGAGCCCTGGAGACA	780						
Qy	1026	GAAGGAGCTGATGGGCACACTTTCGGAGTGCCCTGTTTACCGAGATGGTTGGAGCAGAG	1085						
Db	781	GAAGGAGCTGATGGGCACACTTTCGGAGTGCCCTGTTTACCGAGATGGTTGGAGCAGAG	840						
Qy	1086	TGGATCTTTGGGGTGTGAAATACCAGTATGGTGGCAACCAAGAGGGGAGGTGGGCTTT	1145						
Db	841	TGGATCTTTGGGGTGTGAAATACCAGTATGGTGGCAACCAAGAGGGGAGGTGGGCTTT	900						
Qy	1146	GAGCCCTGCTATGCCGAAGTGTGAGGGTGGTACGAGGAAAACCTTCAACGACGAGGAG	1205						
Db	901	GAGCCCTGCTATGCCGAAGTGTGAGGGTGGTACGAGGAAAACCTTCAACGACGAGGAG	960						
Qy	1206	GTCCAGAGAGGTTCTCTTCTATGCTTTCTCTTACTATTATGACCGAGCTGTTGACACAG	1265						

Db	961	GTCCAGAGAGGTTCTTCTATGCTTTCTCTTACTATTATGACCGAGCTGTTGACACAGAC	1020						
Qy	1266	ATGATTGATTATGAAAAGGGGGGTATTTTAAAGTTGAAGATTTTGAAGAAAAGCCAGG	1325						
Db	1021	ATGATTGATTATGAAAAGGGGGGTATTTTAAAGTTGAAGATTTTGAAGAAAAGCCAGG	1080						
Qy	1326	GAAGTGTGTGATAACTTGGAAAAACTTCACCTCAGGCAGTCCCTTCCCTGTGCATGGATCTC	1385						
Db	1081	GAAGTGTGTGATAACTTGGAAAAACTTCACCTCAGGCAGTCCCTTCCCTGTGCATGGATCTC	1140						
Qy	1386	AGCTACATCACAGCCCTGTTAAAGGATGGCTTTGGCTTTTGACAGACAGACAGTCTTACAG	1445						
Db	1141	AGCTACATCACAGCCCTGTTAAAGGATGGCTTTGGCTTTTGACAGACAGACAGTCTTACAG	1200						
Qy	1446	CTCACAAGAAAGTGAACAACATAGAGACGGGCTGGGCCCTTGGGGGCCACCTTTACACCTG	1505						
Db	1201	CTCACAAGAAAGTGAACAACATAGAGACGGGCTGGGCCCTTGGGGGCCACCTTTACACCTG	1260						
Qy	1506	TTGCAGTCTCTGGGCATCTCCCAATTGA	1532						
Db	1261	TTGCAGTCTCTGGGCATCTCCCAATTGA	1287						
RESULT 10									
US-10-091-085-6									
; Sequence 6, Application US/10091085									
; Publication No. US20020146772A1									
; GENERAL INFORMATION:									
; APPLICANT: Ford, John									
; APPLICANT: Mulero, Julio									
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE									
; TITLE OF INVENTION: POLYPEPTIDES									
; FILE REFERENCE: 28110/35761									
; CURRENT APPLICATION NUMBER: US/10/091,085									
; CURRENT FILING DATE: 2002-03-05									
; PRIOR APPLICATION NUMBER: 09/350,836									
; PRIOR FILING DATE: 1999-07-09									
; PRIOR APPLICATION NUMBER: 09/273,447									
; PRIOR FILING DATE: 1999-03-19									
; PRIOR APPLICATION NUMBER: 09/118,205									
; PRIOR FILING DATE: 1998-07-16									
; PRIOR APPLICATION NUMBER: 09/122,449									
; PRIOR FILING DATE: 1998-07-24									
; PRIOR APPLICATION NUMBER: 09/244,444									
; PRIOR FILING DATE: 1999-02-04									
; NUMBER OF SEQ ID NOS: 23									
; SOFTWARE: PatentIn Ver. 2.0									
; SEQ ID NO 6									
; LENGTH: 1287									
; TYPE: DNA									
; ORGANISM: Homo sapiens									
; FEATURE:									
; NAME/KEY: CDS									
; LOCATION: (1)..(1284)									
US-10-091-085-6									
Query Match 71.0%; Score 1277.4; DB 13; Length 1287;									
Best Local Similarity 99.5%; Pred. No. 0;									
Matches 1281; Conservative 0; Mismatches 6; Indels 0; Gaps 0;									
Qy	246	ATGGCCACTTCTTGGGGCACAGTCTTTTTCATGCTGGTGGTATCCTGTGTTTCAGCGCT	305						
Db	1	ATGGCCACTTCTTGGGGCACAGTCTTTTTCATGCTGGTGGTATCCTGTGTTTCAGCGCT	60						
Qy	306	GTCTCCACAGGAACCCAGCAGACTTGGTTTGAGGGTATCTTCTGTCTTCCATGTGCCCC	365						
Db	61	GTCTCCACAGGAACCCAGCAGACTTGGTTTGAGGGTATCTTCTGTCTTCCATGTGCCCC	120						
Qy	366	ATCAATGTCAGCGCCAGCACCTTGTATGGAATATGTTTGTATGCAGGAGCACTGGAACT	425						
Db	121	ATCAATGTCAGCGCCAGCACCTTGTATGGAATATGTTTGTATGCAGGAGCACTGGAACT	180						
Qy	426	CGAATTCATGTTTACACCTTTGTGCAGAAAATGCCAGGACAGCTTCCAAATCTAGAGGG	485						

181 CGAATTCATGTTTACACCTTTGTGCAGAAAATGCCAGGACAGCTTCCAATTCTAGAAGGG 240
486 GAAGTTTTGATTCTGTGAAGCCAGGACTTCTGCTTTTGTAGATCAACCTAAGCAGGGT 545
242 GAAGTTTTGATTCTGTGAAGCCAGGACTTCTGCTTTTGTAGATCAACCTAAGCAGGGT 300
546 GCTGAGACCGTTCAAGGGCTCTTAGAGGTGGCCAAAGACTCAATCCCCCGAAGTCACTGG 605
301 GCTGAGACCGTTCAAGGGCTCTTAGAGGTGGCCAAAGACTCAATCCCCCGAAGTCACTGG 360
606 AAAAAGACCCCAAGTGGTCCCTAAAGGCCAACAGCAGGACTACGCTTACTGCCAGAACACAAA 665
362 AAAAAGACCCCAAGTGGTCCCTAAAGGCCAACAGCAGGACTACGCTTACTGCCAGAACACAAA 420
666 GCCAAGGCTCTGCTCTTTGAGGTAAAGGAGATCTTCAGAAAGTCAACCTTTCCTGGTACCA 725
421 GCCAAGGCTCTGCTCTTTGAGGTAAAGGAGATCTTCAGAAAGTCAACCTTTCCTGGTACCA 480
726 AAGGCAGTGTTAGCATCATGGATGGATCCGACGAAGGCATATTAGCTTGGGTACTGTG 785
481 AAGGCAGTGTTAGCATCATGGATGGATCCGACGAAGGCATATTAGCTTGGGTACTGTG 540
786 AATTCTTGACAGGTCACTGCTGATGCCACAGACAGGAGACTGTGGGACCTTGGACCTA 845
541 AATTCTTGACAGGTCACTGCTGATGCCACAGACAGGAGACTGTGGGACCTTGGACCTA 600
846 GGGGAGCCTCCACCCAAATCAGCTTCCTGCCCCAGTTTGAGAAACTCTGGAACAAACT 905
601 GGGGAGCCTCCACCCAAATCAGCTTCCTGCCCCAGTTTGAGAAACTCTGGAACAAACT 660
906 CCTAGGGGCTACCTCACTTCCTTTGAGATGTTTAAACAGCACTTATAAGCTCTATACAT 965
661 CCTAGGGGCTACCTCACTTCCTTTGAGATGTTTAAACAGCACTTATAAGCTCTATACAT 720
966 AGTTACCTGGGATTTGGATTGAAAGCTGCAAGACTAGCAACCCCTGGAGCCCTGGAGACA 1025
721 AGTTACCTGGGATTTGGATTGAAAGCTGCAAGACTAGCAACCCCTGGAGCCCTGGAGACA 780
1026 GAAGGGACTGATGGGCACACTTTCGGAGTGCCCTGTTTACCGAGATGGTTGGAAGCAGAG 1085
781 GAAGGGACTGATGGGCACACTTTCGGAGTGCCCTGTTTACCGAGATGGTTGGAAGCAGAG 840
1086 TGGATCTTTGGGGGTGTGAATACCACTATGGTGGCMAACCAAGAGGGGAGGTGGGCTTT 1145
841 TGGATCTTTGGGGGTGTGAATACCACTATGGTGGCMAACCAAGAGGGGAGGTGGGCTTT 900
1146 GAGCCTGCTATGCCGAAGTGTGAGGGTGGTACGAGGAAACTTCACCAGCCAGAGGAG 1205
901 GAGCCTGCTATGCCGAAGTGTGAGGGTGGTACGAGGAAACTTCACCAGCCAGAGGAG 960
1206 GTCCAGAGAGGTTCCTTCTATGCTTCTTACTATTATGACCGAGCTGTTGACACAGAC 1265
961 GTCCAGAGAGGTTCCTTCTATGCTTCTTCTTACTATTATGACCGAGCTGTTGACACAGAC 1020
1266 ATGATTGATTATGAAAAGGGGGTATTTTAAAAGTTGAAGATTTTGAAGAGAAAAGCCAGG 1325
1021 ATGATTGATTATGAAAAGGGGGTATTTTAAAAGTTGAAGATTTTGAAGAGAAAAGCCAGG 1080
1326 GAAGTGTGTGATAACTTGGAAAACCTTCACCTCAGGCACTCTTTCCTGTGCAATGGATCTC 1385
1081 GAAGTGTGTGATAACTTGGAAAACCTTCACCTCAGGCACTCTTTCCTGTGCAATGGATCTC 1140
1386 AGCTACATCACAGCCCTGTTAAAGGATGGCTTTGGCTTTGCAGACAGCACAGTCTTACAG 1445
1141 AGCTACATCACAGCCCTGTTAAAGGATGGCTTTGGCTTTGCAGACAGCACAGTCTTACAG 1200
1446 CTCACAAAGAAAGTGAACAACATAGACAGGGCTGGGCTTGGGGCCACCTTTCACCTG 1505
1201 CTCACAAAGAAAGTGAACAACATAGACAGGGCTGGGCTTGGGGCCACCTTTCACCTG 1260
1506 TTGCAGTCTCTGGGCATCTCCCATTTGA 1532

Db 1261 TTGCAGTCTCTGTGGGCATCTCCCATTTGA 1287

RESULT 11
US-10-092-063-6
; Sequence 6, Application US/10092063
; Publication No. US20020173005A1
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE POLYPEPTIDES
; FILE REFERENCE: 28110/35908
; CURRENT APPLICATION NUMBER: US/10/092,063
; CURRENT FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1287
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; .NAME/KEY: CDS
; LOCATION: (1)..(1284).
US-10-092-063-6

Query Match 71.0%; Score 1277.4; DB 13; Length 1287;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1281; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 246 ATGGCCACTTCTTGGGGCACAGCTCTTTTTCATGCTGTGTGTGTATCCTGTGTGTGTGACGGCT 305
Db 246 ATGGCCACTTCTTGGGGCACAGCTCTTTTTCATGCTGTGTGTGTATCCTGTGTGTGTGACGGCT 60
QY 306 GTCTCCACAGGAACCCAGCAGACTTGGTTTGAGGGTATCTTCTGTCTTCCATGTGCCCC 365
Db 61 GTCTCCACAGGAACCCAGCAGACTTGGTTTGAGGGTATCTTCTGTCTTCCATGTGCCCC 120
QY 366 ATCAATGTGAGCGCCAGCACCTTGTATGGAATTATGTTGATGCAGGGAGCACTGGAACT 425
Db 121 ATCAATGTGAGCGCCAGCACCTTGTATGGAATTATGTTGATGCAGGGAGCACTGGAACT 180
QY 426 CGAATTCATGTTTACACCTTGTGCAGAAAATGCCAGACAGCTTCCAATTCCTAGAGGG 485
Db 181 CGAATTCATGTTTACACCTTGTGCAGAAAATGCCAGACAGCTTCCAATTCCTAGAGGG 240
QY 486 GAAGTTTTGATTCTGTGAAGCCAGGACTTTCGCTTTTGTAGATCAACCTAAGCAGGGT 545
Db 241 GAAGTTTTGATTCTGTGAAGCCAGGACTTTCGCTTTTGTAGATCAACCTAAGCAGGGT 300
QY 546 GCTGAGACCGTTCAAGGGCTCTTAGAGGTGGCCAAAGACTCAATCCCCCGAAGTCACTGG 605
Db 301 GCTGAGACCGTTCAAGGGCTCTTAGAGGTGGCCAAAGACTCAATCCCCCGAAGTCACTGG 360
QY 606 AAAAAGACCCCAAGTGGTCTTAAAGGCCAACAGCAGGACTACGCTTACTGCCAGAACACAAA 665
Db 361 AAAAAGACCCCAAGTGGTCTTAAAGGCCAACAGCAGGACTACGCTTACTGCCAGAACACAAA 420
QY 666 GCCAAGGCTCTGCTCTTTGAGGTAAAGGAGATCTTCAGSAAAGTCACTTTCCTGGTACCA 725

Db 421 GCCAAGGCTCTGCTCTTTGAGGTAAAGGAGATCTTCAGGAATCACCCTTCCTGGTACCA 480
2Y 726 AAGGGCAGTGTAGCATCATGGATGATCCGACGAAGGCATATTAGCTTGGGTTACTGTG 785
Db 481 AAGGGCAGTGTAGCATCATGACTGACACAGACGAAGGCATATTGCTTGGGTTACTGTG 540
2Y 786 AATTCTCTGACAGGTCAGCTGCATGGCCACAGACAGGAGACTGTGGGACCTTGGACCTA 845
Db 541 AATTCTCTGACAGGTCAGCTGCATGGCCACAGACAGGAGACTGTGGGACCTTGGACCTA 600
2Y 846 GGGGGAGCCTCCACCCAAATCACGTTCTGCCCCAGTTTGAAGAAACTCTGGAACAACT 905
Db 601 GGGGGAGCCTCCACCCAAATCACGTTCTGCCCCAGTTTGAAGAAACTCTGGAACAACT 660
2Y 906 CCTAGGGGTACCTCACTTCCTTTGAGATGTTTAAACAGCACTTATAAGCTCTATACACAT 965
Db 661 CCTAGGGGTACCTCACTTCCTTTGAGATGTTTAAACAGCACTTATAAGCTCTATACACAT 720
Y 966 AGTTACCTGGGATTTGGATTGAAGCTGCAAGACTAGCAACCTGGGAGCCCTGGAGACA 1025
Db 721 AGTTACCTGGGATTTGGATTGAAGCTGCAAGACTAGCAACCTGGGAGCCCTGGAGACA 780
2Y 1026 GAAGGGACTGATGGGCACACTTTCGGAGTGCCTGTTTACCGAGATGTTTGAAGCAGAG 1085
Db 781 GAAGGGACTGATGGGCACACTTTCGGAGTGCCTGTTTACCGAGATGTTTGAAGCAGAG 840
2Y 1086 TGGATCTTTGGGGGTGTGAAATACCACTATGGTGGCAACCAAGAAAGGGAGGTGGGCTTT 1145
Db 841 TGGATCTTTGGGGGTGTGAAATACCACTATGGTGGCAACCAAGAAAGGGAGGTGGGCTTT 900
2Y 1146 GAGCCCTGCTATGCCGAAGTCTGAGGGTGTACGAGGAAACTTCACCAGCCAGAGGAG 1205
Db 901 GAGCCCTGCTATGCCGAAGTCTGAGGGTGTACGAGGAAACTTCACCAGCCAGAGGAG 960
Y 1206 GTCCAGAGAGGTTCTTCTATGCTTCTTACTATTATGACCGAGCTGTGACACAGAC 1265
b 961 GTCCAGAGAGGTTCTTCTATGCTTCTTACTATTATGACCGAGCTGTGACACAGAC 1020
Y 1266 ATGATTGATTATGAAAAGGGGGGATTTTAAAAGTTGAGATTTTGAAGAAAGCCAGG 1325
b 1021 ATGATTGATTATGAAAAGGGGGGATTTTAAAAGTTGAGATTTTGAAGAAAGCCAGG 1080
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b 1081 GAAGTGCTGATAACTTGGAAAACCTTCACCTCAGGCAGTCTTCCCTGTGCAATGGATCTC 1140
Y 1386 AGCTACATCACAGCCCTGTTAAAGGATGGCTTTGGCTTTGCGAGACAGCAGTCTTACAG 1445
b 1141 AGCTACATCACAGCCCTGTTAAAGGATGGCTTTGGCTTTGCGAGACAGCAGTCTTACAG 1200
Y 1446 CTCACAAAGAAAGTGAACAACATAGAGACGGGCTGGGCCCTTGGGGCCACCTTTACCTG 1505
b 1201 CTCACAAAGAAAGTGAACAACATAGAGACGGGCTGGGCCCTTGGGGCCACCTTTACCTG 1260
Y 1506 TTGCAGTCTCTGGGCATCTCCCATTTGA 1532
b 1261 TTGCAGTCTCTGGGCATCTCCCATTTGA 1287

RESULT 12

S-09-925-299-103
Sequence 103, Application US/09925299
Patent No. US20020055627A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA102
CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12

; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 103
; LENGTH: 1457
; TYPE: DNA
; ORGANISM: Homo sapiens
JS-09-925-299-103
Query Match 60.5%; Score 1089.2; DB 9; Length 1457;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 1085; Conservative 9; Mismatches 2; Indels 0; Gaps 0;
QY 553 CCGTTCAGGGCTCTTAGAGGTGGCCAAAGACTCAATCCCGGAAGTCACTGGAAAAAGA 612
Db 14 CCGTTCAGGGCTCTTAGAGGTGGCCAAAGACTCAATCCCGGAAGTCACTGGAAAAAGA 73
QY 613 CCCAGTGTCTCTAAAGGCAACAGCAGGACTACGCTTACTGCCAGAACACAAAGCCAAGG 672
Db 74 CCCAGTGTCTCTAAAGGCAACAGCAGGACTACGCTTACTGCCAGAACACAAAGCCAAGG 133
QY 673 CTCTGCTCTTTGAGGTAAGGAGATCTTCAGGAAGTCACTTTCCCTGGTACCAAGGGCA 732
Db 134 CTCTGCTCTTTGAGGTAAGGAGATCTTCAGGAAGTCACTTTCCCTGGTACCAAGGGCA 193
QY 733 GTGTTAGCATCATGGATGGATCCGACGAAGGCATATTAGCTTGGGTTACTGTGAATTTTC 792
Db 194 GTGTTAGCATCATGGATGGATCCGACGAAGGCATATTAGCTTGGGTTACTGTGAATTTTC 253
QY 793 TGACAGGTCACTGCATGGCCACAGACAGGAGACTGTGGGACCTTGGACCTAGGGGAG 852
Db 254 TGACAGGTCACTGCATGGCCACAGACAGGAGACTKTGGGACCTTGGACCTAGGGGAG 313
QY 853 CCTCCACCCAAATCACGTTTCCTGCCCCAGCTTGAGAAACTCTGGAACAAACTCCTAGGG 912
Db 314 CCTYACCCAAATCACGTTTCCTGCCCCAGCTTGAGAAACTCTGGAACAAACTCCTAKGS 373
QY 913 GCTACCTCACTTCCTTTGAGATGTTTAAACAGCACTTATAAGCTCTATACACATAGTTACC 972
Db 374 GCTACCTCACTTCCTTTGAGATGTTTAAACAGCACTTATAAGCTCTATACACATAGTTACT 433
QY 973 TGGGATTTGGATTGAAAGCTGCAAGACTAGCAACCCCTGGGAGCCCTGGAGACGAGAGGGA 1032
Db 434 TGGGATTTGGATTGAAAGCTGCAAGACTAGCAACCCCTGGGAGCCCTGGAGACGAGAGGGA 493
QY 1033 CTGATGGGCACACTTTCGGAGTGCCTGTTTACCAGATGGTGGTGGAGCAGAGTGGATCT 1092
Db 494 CTGATGGGCACACTTTCGGAGTGCCTKTTTACCAGATGKTTTGAAGCAGAGTGGATCT 553
QY 1093 TTGGGGTGTGAAATACCAATATGGTGGCAACCAAGAGGSGAGGTGGCTTTGAGCCCT 1152
Db 554 TTGGGGTGTGAAATACCAATATGGTGGCAACCAAGAGGSGAGGTGGCTTTGAGCCCT 613
QY 1153 GCTATGCCGAAGTGTCTGAGGGTGGTACGAGGAAAACTTACCAGCCAGAGGAGGTCCAGA 1212
Db 614 GCTATGCCGAAGTGTCTGAGGGTGGTACGAGGAAAACTTACCAGCCAGAGGAGGTCCAGA 673
QY 1213 GAGGTTCTCTTATGCTTTCTCTTACTATTATGACCGAGCTGTTGACACAGACATGATTG 1272
Db 674 GAGGTTCTCTTATGCTTTCTCTTACTATTATGACCGAGCTGTTGACACAGACATGATTG 733
QY 1273 ATTATGAAAAAGGGGGTATTTTAAAAAGTTGAAGATTTTGAAGAAAGCCAGGGAAGTGT 1332
Db 734 ATTATGAAAAAGGGGGTATTTTAAAAAGTTGAAGATTTTGAAGAAAGCCAGGGAAGTGT 793
QY 1333 GTGATAACTTGGAAAACTTCACCTCAGGCAGTCCCTTCCCTGTGCATGGATCTCAGCTACA 1392
Db 794 GTGATAACTTGGAAAACTTCACCTCAGGCAGTCCCTTCCCTGTGCATGGATCTCAGCTACA 853
QY 1393 TCACAGCCCTGTTAAAGGATGGCTTTGGCTTTGCAGACAGCAGTCTTACAGCTCACAA 1452
Db 854 TCACAGCCCTGTTAAAGGATGGCTTTGGCTTTGCAGACAGCAGTCTTACAGCTCACAA 913
QY 1453 AGAAAGTGAACAACATAGACAGGGGCTGGGCCCTTGGGGGCCACCTTTTCACCTGTTGCAGT 1512

||||| 914 AGAAGTGAACAACATAGAGCGGGCTGGCCCTTGGGGCCACCTTTTCACCTGTGGCAGT 973
Y 1513 CTCTGGGCATCTCCCATTTAGGCCACGTACTTCTCTGGAGACCTGCATTTGGCAACACCT 1572
b 974 CTCTGGGCATCTCCCATTTAGGCCACGTACTTCTCTGGAGACCTGCATTTGGCAACACCT 1033
Y 1573 TTTTAAGGGGAGGAGAGAGCACTTAGTTTCTGAACCTAGTCTGGGGACATCTCTGGACTTGA 1632
b 1034 TTTTAAGGGGAGGAGAGAGCACTTAGTTTCTGAACCTAGTCTGGGGACATCTCTGGACTTGA 1093
Y 1633 GCCTAGAGATTWRGTT 1648
b 1094 GCCTAGAGATTTAGGT 1109
RESULT 13
S-09-925-299-103
Sequence 103, Application US/09925299
Publication No. US20030040617A9
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA102
CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 103
LENGTH: 1457
TYPE: DNA
ORGANISM: Homo sapiens
S-09-925-299-103
Query Match 60.5%; Score 1089.2; DB 11; Length 1457;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 1085; Conservative 9; Mismatches 2; Indels 0; Gaps 0;
Y 553 CCGTTCAAGGGCTCTTAGAGGTGGCCAAAGACTCAATCCCCCGAAGTCACTGGGAAAAAGA 612
b 14 CCGTTCAAGGGCTCTTAGAGGTGGCCAAAGACTCAATCCCCCGAAGTCACTGGGAAAAAGA 73
Y 613 CCCAGTGGTCTTAAGGCAACAGCAGGACTACGTTACTTGGCAGAAACACAAAGCAAGG 672
b 74 CCCAGTGGTCTTAAGGCAACAGCAGGACTACGTTACTTGGCAGAAACACAAAGCAAGG 133
Y 673 CTCTGCTCTTTGAGGTAAAGGAGATCTTCAGGAAGTCACCTTTCCTGGTACCAAGGGCA 732
b 134 CTCTGCTCTTTGAGGTAAAGGAGATCTTCAGGAAGTCACCTTTCCTGGTACCAAGGGCA 193
Y 733 GTGTTAGCATCATGGATGGATCCGACGAAGGCATATTAGCTTGGGTTACTGTGAATTTTC 792
b 194 GTGTTAGCATCATGGATGGATCCGACGAAGGCATATTAGCTTGGGTTACTGTGAATTTTC 253
Y 793 TGACAGGTCAGCTGCATGGCCACACACAGGAGACTGTGGGACCTTGGACCTAGGGGGAG 852
b 254 TGACAGGTCAGCTGCATGGCCACACACAGGAGACTKTGGGACCTTGGACCTAGGGGGAG 313
Y 853 CCTCCACCCAAATCACGTTTCCTGCCCCAGTTTGAGAAAACCTCTGGAAACAACTCTTAGGG 912
b 314 CCTYCACCCAAATCACGTTTCCTGCCCCAGTTTGAGAAAACCTCTGGAAACAACTCTTAGGG 373
Y 913 GCTACCTCACTTCCTTTGAGATGTTTAAACAGCACTTATAAGCTCTATACACATAGTTACC 972
b 374 GCTACCTCACTTCCTTTGAGATGTTTAAACAGCACTTATAAKTCTATACACATAGTTACT 433
Y 973 TGGGAFTTGGATTGAAGCTGCAAGACTAGCAACCCCTGGGAGCCCTGGAGACAGAGGGA 1032
b 434 TGGGATTTGSAATTGAAGCTGCAAGACTAGCAACCCCTGGGAGCCCTGGAGACAGAGGGA 493

QY 1033 CTGATGGGCACACACTTTCGGAGTGCCTGTGTTTACCGAGATGTTTGGAAAGCAGAGTGGATCT 1092
Db 494 CTGATGGGCACACACTTTCGGAGTGCCTKTTTACCAGATGKTTTGGAAAGCAGAGTGGATCT 553
QY 1093 TTGGGGGTGTGAATATACCACTATGGTGGCAACCAAGAGGGGAGGTGGGCTTTGAGCCCT 1152
Db 554 TTGGGGGTGTGAATATACCACTATGGTGGCAACCAAGAGGGGAGGTGGGCTTTGAGCCCT 613
QY 1153 GCTATGCCGAAGTGCTGAGGTGGTACGAGGAAAACCTTACCAGCCAGAGGAGGTCCAGA 1212
Db 614 GCTATGCCGAAGTGCTGAGGTGGTACGAGGAAAACCTTACCAGCCAGAGGAGGTCCAGA 673
QY 1213 GAGGTTCTTCTATGCTTTCTCTTACTATTATGACCAGCTGTGACACAGACATGATTG 1272
Db 674 GAGGTTCTTCTATGCTTTCTCTTACTATTATGACCAGCTGTGACACAGACATGATTG 733
QY 1273 ATTATGAAAAGGGGGTATTTTAAAGTTGAAGATTTTGAAGAAAAGCCAGGGAAGTGT 1332
Db 734 ATTATGAAAAGGGGGTATTTTAAAGTTGAAGATTTTGAAGAAAAGCCAGGGAAGTGT 793
QY 1333 GTGATAACTTGGAAAACCTTCACCTCAGGCAGTCCTTCTCTGTCATGGATCTCAGTACA 1392
Db 794 GTGATAACTTGGAAAACCTTCACCTCAGGCAGTCCTTCTCTGTCATGGATCTCAGTACA 853
QY 1393 TCACAGCCCTGTTAAAGGATGGCTTTGGCTTTTGACAGACAGCAGTCTTACAGCTCACA 1452
Db 854 TCACAGCCCTGTTAAAGGATGGCTTTGGCTTTTGACAGACAGCAGTCTTACAGCTCACA 913
QY 1453 AGAAAGTGAACAACATAGAGCGGGCTGGGCCTTGGGGCCACCTTTTACACCTGTTGAGT 1512
Db 914 AGAAAGTGAACAACATAGAGCGGGCTGGGCCTTGGGGCCACCTTTTACACCTGTTGAGT 973
QY 1513 CTCTGGGCATCTCCCATTTAGGCCACGTACTTCTCTTGAGACCTGCAATTGGCAACACCT 1572
Db 974 CTCTGGGCATCTCCCATTTAGGCCACGTACTTCTCTTGAGACCTGCAATTGGCAACACCT 1033
QY 1573 TTTTAAGGGGAGGAGAGACACTTAGTTTCTGAACCTAGTCTGGGACATCTCTGGACTTGA 1632
Db 1034 TTTTAAGGGGAGGAGAGACACTTAGTTTCTGAACCTAGTCTGGGACATCTCTGGACTTGA 1093
QY 1633 GCCTAGAGATTWRGTT 1648
Db 1094 GCCTAGAGATTTAGGT 1109
RESULT 14
US-10-198-846-12729
; Sequence 12729, Application US/10198846
; Publication No. US2003009974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steinmann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12729
; LENGTH: 978
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 683, 689, 978
; OTHER INFORMATION: n = A,T,C or G

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

M nucleic - nucleic search, using sw model
run on: October 6, 2003, 10:57:37 ; Search time 2687 Seconds
(without alignments)
16272.331 Million cell updates/sec

itle: US-10-092-063-2
erfect score: 1799
equence: 1 ggggctgcgcgcgaagggt.....cgacgccttcacagtgccca 1799

oring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0
eached: 22781392 seqs, 12152238056 residues
otal number of hits satisfying chosen parameters: 45562784

inimum DB seq length: 0
aximum DB seq length: 2000000000
ost-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

atabase : EST:
1: em_estba:*
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4: em_estmu:*
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6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
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16: em_estom:*
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21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Match	Length	DB ID	Description
1	1085.4	60.3	3698	11	AK080265 Mus muscu
2	1084	60.3	4014	11	AK081435 Mus muscu
3	1083.8	60.2	4091	11	AK036641 Mus muscu
4	1082.2	60.2	2517	11	AK031581 Mus muscu

5	1081.4	60.1	2124	11	AK088455
6	1065.6	59.2	1661	11	AK079267
7	1064.4	59.2	1861	11	AK037736
8	1063.2	59.1	2070	11	AK002618
9	1059.2	58.9	4884	11	AK045828
10	882.4	49.0	1107	12	BM924818
11	761.4	42.3	842	12	BI258902
12	692.6	38.5	749	12	BI765978
13	681	37.9	801	12	BI551795
14	649	36.1	878	10	BG702864
15	636.4	35.4	881	12	BG969449
16	603.4	33.5	825	12	BI256038
17	561.8	31.2	577	10	BE780916
18	514	28.6	514	14	CB132043
19	499.6	27.8	610	10	BG064462
20	481.2	26.7	559	14	CB163434
21	478.6	26.6	785	13	BU469055
22	478.6	26.6	1106	10	BF780434
23	477	26.5	832	13	BU468983
24	474.4	26.4	902	10	BG433545
25	467.8	26.0	527	10	BF073260
26	465.8	25.9	542	9	AW785380
27	463.4	25.8	965	10	BF687132
28	458.2	25.5	777	12	BG971749
29	458	25.5	537	10	BE397644
30	454.8	25.3	965	13	BU397374
31	454.2	25.2	526	10	BE750917
32	451	25.1	547	9	AW544751
33	446.4	24.8	864	12	BI217588
34	431.6	24.0	668	10	BB611968
35	431.2	24.0	828	13	BU471848
36	423.2	23.5	656	9	AW611029
37	411	22.8	411	14	CB132877
38	407.2	22.6	598	14	BY722223
39	405.8	22.6	881	13	BO717053
40	403.6	22.4	1108	10	BF781939
41	403.4	22.4	756	10	BF786758
42	393.6	21.9	485	14	CB156899
43	382.6	21.3	523	12	EG972646
44	381.2	21.2	941	14	BY703126
45	379.6	21.1	684	10	BB648443

ALIGNMENTS

RESULT 1	AK080265	AK080265	3698 bp	mRNA	linear	HTC 05-DEC-2002
AK080265	Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A630007L13 product:ectonucleoside triphosphate diphosphohydrolase 5, full insert sequence.	Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A630007L13 product:ectonucleoside triphosphate diphosphohydrolase 5, full insert sequence.				
LOCUS	AK080265	AK080265.1	GI:26348444			
DEFINITION	HTC; CAP trapper.	HTC; CAP trapper.				
ACCESSION	AK080265	AK080265				
VERSION	AK080265.1	AK080265.1				
KEYWORDS	Mus musculus (house mouse)	Mus musculus (house mouse)				
SOURCE	Mus musculus	Mus musculus				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
REFERENCE	1	1				
AUTHORS	Carninci,P. and Hayashizaki,Y.	Carninci,P. and Hayashizaki,Y.				
TITLE	High-efficiency full-length cDNA cloning	High-efficiency full-length cDNA cloning				
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)	Meth. Enzymol. 303, 19-44 (1999)				
MEDLINE	99279253	99279253				
PUBMED	10349636	10349636				
REFERENCE	2	2				
AUTHORS	Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.	Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.				
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes				
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)	Genome Res. 10 (10), 1617-1630 (2000)				
MEDLINE	20499374	20499374				
PUBMED	11042159	11042159				

553 CCGTTCAAGGGCTCTTAGAGGTGGCCAAAGACTCAATCCCCGGAAGTCACTGGAAAAAGA 612
561 CTGTCCAGGAGCTCTGGAGGTGGCCAAAGACTCGATCCCCAGAAAGCCACTGGGAAAGGA 620
613 CCCAGTGGTCTTAAAGGCAACAGCAGGACTACGCTTACTGCCAGAACACAAAGCCAAAGG 672
621 CCCGGTGGTCTTGAAGCAACGGCCGGACTCCGTTTGCTGCCTGAGCAGAAAGCCCAAG 680
673 CTCTGCTCTTTGAGTAAAGGAGATCTTCAGGAAGTCACTTTCCCTGGTACCAAAGGGCA 732
681 CTCTGCTCTTGGAGTAGAGGAGATCTTCAAGAAATCACCTTTCCCTGGTCCCAGATGGCA 740
733 GTGTTAGCATCATGGATGGATCCGACGAGGCATPATTAGCTTGGGTTACTGTGAATTTTC 792
741 CGGTTAGCATCATGGATGGTCCCTATGAAGGCATACTAGCCTGGGTTACCTGAACTTTC 800
793 TGACAGGTCAGCTGCATGGCCACAGACAGGAGACTGTGGGGACCTTGGACCTAGGGGGAG 852
801 TAACAGGTCAGCTGCATGGTGTGGCCAGGAGACTGTGGGGACCCCTTGACCTGGGGGGTG 860
853 CCTCCACCCCAATCACGTTCTCTGCCCCAGTTTGAGAAAACTCTGGAACAAACTCCTTAGGG 912
861 CCTCCACCCCAATCACGTTTCTACCCCCAGTTTGAGAAAAACCTTGGAAACAACACCTAGGG 920
913 GCTACCTCACTTCTCTGAGATGTTTAAACAGCACTTATAAGCTCTATACACATAGTTACC 972
921 GCTACCTCACTTCTCTGAGATGTTTAAACAGCACTTTTAAAGCTCTATACACATAGTTACT 980
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981 TGGGATTTGGACTGAAAGTSCAAGACTGGCAACTCTGGGAGCCCTGGAGCAAAAGGGA 1040
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1041 CTGATGGACATACGTTTCAAGTGCCTGTTTACCAGATGGTTTGGAGCAGAGTGGATCT 1100
1093 TTGGGGGTGTGAATACCAATACCAATGTTGGTGCAACCAAGAGGGAGGTGGGCTTTGAGCCCT 1152
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1153 GCTATGCCGAAGTCTGAGGGTGTACGAGGAATTTCAAGAACTTCAACAGCCAGAGAGGTCCAGA 1212
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1213 GAGGTTCCCTTCTATGCTTTCTTACTATTATGACGAGCTGTTGACACACACATGATTG 1272
1221 GAAGCGCCTTCTACGCTTTCTCTTACTACTACGATGAGCGCGCTGACACACACTTGATCG 1280
1273 ATTATGAAAGGGGGTATTTTAAAGTTGAAGATTTGAAGAAATTTGAAGAAAGCCAGGAAGTGT 1332
1281 ATTATGAAAGGGCGGGGTTTAAAGTTGAAGATTTGAAGATTTGAAGAAAGCCAGGAAGTGT 1340
1333 GTGATAACTTGGAAAACITTCACCTCAGGCAGTCCCTTCTCTGTGCATGGATCTCAGCTACA 1392
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1393 TCACAGCCCTGTTAAAGGATGGCTTTTGGCTTTGCAGACAGCAGATCTTACAGCTCACAA 1452
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1461 AGAAGTGAACAACATAGAGACTGGTGGGCTTGGGCTTGGGGCCACCTTTTCACCTGTTCCAGT 1520
1513 CTCTGGGCATCTCCCATTAGGCCACGTACTTCTCTTGAGACCTGCAATTTGCCAACACCT 1572
1521 CTCTGGGCATCACCAGCTGAGCCCAAGCTCCACCTCTGAAGCCTGCATTTCTGAACAGTT 1580
1573 TTTTAAGGGGAGG 1585
1581 TTCTCACAGGAAG 1593

RESULT 2
AK081435
LOCUS
DEFINITION
AK081435 4014 bp mRNA linear HTC 05-DEC-2002
Mus musculus 16 days embryo head cDNA, RIKEN full-length enriched
library, clone:Cl30017F05 product:ectonucleoside triphosphate
diphosphohydrolase 5, full insert sequence.
ACCESSION
AK081435 GI:26349158
VERSION
HTC; CAP trapper.
KEYWORDS
Mus musculus (house mouse)
SOURCE
Mus musculus
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1
Carninci, P. and Hayashizaki, Y.
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JOURNAL
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JOURNAL
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MEDLINE
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PUBMED
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Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishire, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwaki, S., Inoue, K., Togawa, Y., Izawa, M., Chara, E., Watahiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
JOURNAL
20530913
MEDLINE
11076861
PUBMED
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Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, Y., Ishii, Y.,
Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S.,
Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I.,
Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R.,
Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T.,
Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H.,
Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G.,
Quackenbush, J., Schriml, L.M., Staubli, F., Suzuki, R., Tomita, M.,
Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H.,
Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N.,
Carninci, P., de Bonaldo, M.F., Brownstein, M.C., Bult, C.,
Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D.,
Hcfmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P.,
Marchionni, L., Mashima, J., Mazzarelli, C., Mommaerts, P., Nordone, P.,
Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H.,
Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H.,
Toyooka, K., Wang, K.H., Weitz, C., Whittaker, C., Wilming, L.,
Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohetsuki, S.
and Hayashizaki, Y.
Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)
JOURNAL
21085660
MEDLINE
11217851
PUBMED
5
The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
JOURNAL
6 (bases 1 to 4014)
REFERENCE
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,

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1554 CAGTTTCTCACAGGAAG 1571

AK036641 4091 bp mRNA linear HTC 05-DEC-2002

Mus musculus adult male bone cDNA, RIKEN full-length enriched library, clone:9830-44N04 product:ectonucleoside triphosphate diphosphohydrolase 5, full insert sequence.

AK036641 AK036641.1 GI:26331569

HTC; CAP trapper.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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20530913

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Direct Submission

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL:http://genome.gsc.riken.go.jp/

URL:http://fantom.gsc.riken.go.jp/.

Location/Qualifiers

1. 4091

/organism="Mus musculus"

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/db_xref="taxon:10090"

/clone="9830144N04"

/sex="male"

/tissue type="bone"

/clone_lib="RIKEN full-length enriched mouse cDNA library"

/dev_stage="adult"

247. 1530

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/codon_start=1

/protein_id="BAC29515.1"

/db_xref="GI:26331570"

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CDS

PUBMED
REFERENCE
AUTHORS

11042159
3
Shibata,K., Itoh,M., Aizawa,K., Nagacka,S., Sasaki,N., Carrinci,P.,
Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
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Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
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Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H.,
Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G.,
Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M.,
Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H.,
Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N.,
Carrinci,P., de Bonaldo,M.F., Brownstein,M.J., Buit,C.,
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Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,J.,
Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kottzuki,S.
and Hayashizaki,Y.
Functional annotation of a full-length mouse cDNA collection
Nature 409 (6921), 685-690 (2001)
21085660
11217851

TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS

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Matches 1289; Conservative 0; Mismatches 268; Indels 16; Gaps 3;

TITLE

The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 2517)

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REFERENCE
AUTHORS

Agachi,J., Aizawa,K., Akimura,T., Arakawa,T., Benno,H., Carrinci,P.,
Fukuda,S., Furuno,M., Haragaki,T., Hara,A., Hashizume,W.,
Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
Kato,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
Nakamura,K., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
Okazaki,Y., Saito,K., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
Yuramatsu,M. and Hayashizaki,Y.
Direct Submission
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URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)

TITLE
JOURNAL

Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.

COMMENT

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ACCESSION
VERSION
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SOURCE
ORGANISM

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Mus musculus

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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;

REFERENCE

Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
10349636

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Sumi, N., Ishii, Y., Nakamura, S., Hazama, N., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
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RIKEN integrated sequence analysis (RISA) system--384-format
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JOURNAL
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AUTHORS

Functional annotation of a full-length mouse cDNA collection
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REFERENCE

The FANTOM Consortium and the RIKEN Genome Exploration Research
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TITLE

Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

6 (bases 1 to 2124)
REFERENCE Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Boto,H., Carninci,F.,
AUTHORS Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,N.,
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Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
Muramatsu,M. and Hayashizaki,Y.
Direct Submission
Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
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RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-res@gs.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics
Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome
Trust/MRC building Addenbrookes Hospital Cambridge) whose
assistance we gratefully acknowledge.
Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.

FEATURES

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RIGIN

Query Match 60.1%; Score 1081.4; DB 11; Length 2124;
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LOCUS	AK079267	1661 bp	mRNA
DEFINITION	Mus musculus adult male urinary bladder cDNA, RIKEN full-length enriched library, clone:9530068A17 product:ectonucleoside triphosphate diphosphohydrolase 5, full insert sequence.		
ACCESSION	AK079267		
VERSION	AK079267.1	GI:26347886	
KEYWORDS	HTC; CAP trapper.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	1	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.	
AUTHORS	Carninci, P. and Hayashizaki, Y.		
TITLE	High-efficiency full-length cDNA cloning		
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)		
MEDLINE	99279253		
PUBMED	10349636		
REFERENCE	2		
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itch, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.		
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes		
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)		
MEDLINE	20499374		
PUBMED	11042159		
REFERENCE	3		
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaki, S., Inoue, K., Togawa, Y., Izawa, M., Chara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.		
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer		
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)		
MEDLINE	20530913		
PUBMED	11076861		
REFERENCE	4		
AUTHORS	Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,		

	Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Tomita, M., Quackenbush, J., Schriml, L. M., Staubli, F., Suzuki, R., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seva, T., Shibata, Y., Storch, K. F., Suzuki, H., Toyooka, K., Wang, K. H., Weitz, C., Whittaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S. and Hayashizaki, Y.	
	Functional annotation of a full-length mouse cDNA collection	
	Nature 409 (6821), 685-690 (2001)	
	21085660	
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	5	
	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.	
	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs	
	Nature 420, 563-573 (2002)	
	6 (bases 1 to 1661)	
	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, N., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.	
	Direct Submission	
	Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)	
	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.	
	Please visit our web site for further details.	
	URL: http://genome.gsc.riken.go.jp/	
	URL: http://fantom.gsc.riken.go.jp/	
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	CDS	

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Query Match 59.2%; Score 1065.6; DB 11; Length 1661; Best Local Similarity 85.2%; Pred. No. 2.2e-219; Matches 1215; Conservative 0; Mismatches 204; Indels 7; Gaps 2;

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RESULT 7
AK037736
LOCUS
DEFINITION
Mus musculus 16 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A13004A06 product:ectonucleoside triphosphate diphosphohydrolase 5, full insert sequence.
AK037736
AK037736.1 GI:26332261
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1
Carninci,P. and Hayashizaki,Y.
TITLE
High-efficiency full-length cDNA cloning
JOURNAL
Meth. Enzymol. 303, 19-44 (1999)
MEDLINE
99279253
PUBMED
10349636
2
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL
Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE
20499374
PUBMED
11042159
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Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsuurai,T., Tashiro,H., Itoh,M.,

Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
11076861
4
Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojebori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Bataiov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pescio,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C., Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,Y., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,J., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyooka,K., Wang,K.H., Weitz,C., Whitaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.
Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)
21085660
1217851

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

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JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

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DB 691 TGGGTACCGTGAACCTTTCTAACAGGTGAGCTGATGCTGCTGCGCCAGGAGACTGTGGGG 750

further details.
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken. Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5', GAGAGAGAGCGCGCGCACTCGAGTTTTTTTTTTTTTN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 5.0. Second strand cDNA was prepared with the primer adapter of sequence[5', GAGAGAGAGAGATCCAGAGCTCAATTAATTTAATTAAACCCCCCCCC 3']. cDNA was cleaved with XhoI and SstI. Cloning sites, 5' end: SstI; 3' end: XhoI. Host: SOLR.

FEATURES

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CDS

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BASE COUNT
RIGIN

Query Match 59.1%; Score 1063.2; DB 11; Length 2070;
Best Local Similarity 85.0%; Pred. No. 7.4e-219;
Matches 1215; Conservative 0; Mismatches 208; Indels 7; Gaps 2;
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D 84 CAAAGGGAGGGCCTGAAGGACCTCCACAGGAGTGTGAGCAGCACTGCTTCAGCACAAAA- 142
Y 216 GCCTCCACCCAGCCACATCTTGGGAAAAGAAATGGCCACTTCTTGGGGCACAGTCTTTTC 275
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Mus musculus (house mouse)
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1
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
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2
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
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3
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwaki, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
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4
Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,
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Carninci, P., de Bonaudo, M. F., Brownstein, M. J., Bult, C.,
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Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P.,
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Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H.,
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Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawai, H., Kohtsuki, S.
and Hayashizaki, Y.
Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)
21085660
11217851
5
The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

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REFERENCE.
AUTHORS
6 (bases 1 to 4884)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Haragaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T.,
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Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numata, R., Ohno, M., Ohsato, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.
Direct Submission
TITLE
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration and Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)
COMMENT
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.go.jp/
URL: http://fantom.gsc.riken.go.jp/.
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VERSION
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SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

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BM924818.1 GI:19375197
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1 (bases 1 to 1107)
NIH-MGC <http://mgi.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (JLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/JLNL at:
<http://image.llnl.gov>
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1 (bases 1 to 842)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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ORIGIN

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Db 361 TTCCTGCCCCCAGTTTGAGAAACTCTTGGAACTCTAGGGGCTACCTCACTTCCTTT 420
QY 930 GAGATGTTTAAACAGCACTTATAAGCTCTATACATAGTACCTGGGATTTGGATTGAAA 989

REFERENCE 1 (bases 1 to 801)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: Miklos Palokovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM1699 row: m column: 24
High quality sequence stop: 777.

FEATURES
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pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI (gtcgag
); Oligo-dT primed using primer 5'-TTTCTTTTCTTTTCTT-3',
size-selected for average insert size 2.5 kb and
normalized to ROT 5. This is a primary library enriched
for full-length clones and constructed using the
Cap-trapper method (Carninci, in preparation). Library
constructed by M. Brownstein (NIMH/NHGRI, National
Institutes of Health). Note: this is a NIH_MGC Library."

ASE COUNT 212 a 177 c 211 g 201 t
RIGIN

Query Match 37.9%; Score 681; DB 12; Length 801;
Best Local Similarity 95.0%; Pred. No. 2e-136;
Matches 757; Conservative 0; Mismatches 10; Indels 30; Gaps 4;

17 GGGTGGCGCGGGGCTTTCTCTGTTCTGGTCAACAAGAAATGTGGAGTGTCTGGC 76
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b 5 GGGTGGCGCGGGGCTTTCTCTGTTCTGGTCAACAAGAAATGTGGAGTGTCTGGC 64
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77 TGAATCCTCATACAGACAAGATCATTTATGTCGTCTGT----- 113
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65 TGAATCCTCATACAGACAAGATCATTTATGTCGTCTGTAGGTAGGACTTGATCCAGATGT 124
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114 -AGGTTGAAAAAGTGATATAATAAGGACCAAGGAGNATTCAGAAGGAAGAAAAA 172
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125 AAGTTGAAAAAGTGATATAATAAGGACCAAGGAGNATTCAGAAGGAAGAAAAA 184
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173 TTGCCTCTGCAGGTGTGGCAGCAGGATTGCTCTGCAACAAAAGCCTCCACCCAGCCACA 232
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185 TTGCCTCTGCAGGTGTGGCAGCAGGATTGCTCTGCAACAAAAGCCTCCACCCAGCCACT 244
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233 TCTTGGGAAAAGATGGCCCACTTCTTGGGGCACAGTCTTTTTCATGCTGGTATCCCTG 292
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245 TCTTGGGAAAAGATGGCCCACTTCTTGGGGCACAGTCTTTTTCATGCTGGTATCCCTG 304
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353 TTCCATGTGCCCCATCAATGTGAGCCGACCACTTGTATGGAATATGTTGATGCAGG 412
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365 TTCCATGTGCCCCATCAATGTGAGCCGACCACTTGTATGGAATATGTTGATGCAGG 424
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413 GAGCACTGGAACCTCGAATTCATGTTTACACCTTTGTGCAGAAAAATGCCAGGACAGCTCC 472
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425 GAGCACTGGAACCTCGAATTCATGTTTACACCTTTGTGCAGAAAAATGCCAGGACAGCTCC 484
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QY 473 AATTCTAGAAGGGGAAGTTTGTGATCTCTGTGAAGCAGGACTTCTGCTTTGTAGATCA 532
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Db 485 AATTCTAGAAGGGGAAGTTTGTGATCTCTGTGAAGCAGGACTTCTGCTTTGTAGATCA 544
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QY 653 GCCAGAACACAAAGCCAGGCTCTGCTCTTTGAGGTAAAGGAGATCTTCA-GGAAGTCAC 711
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Db 665 GCCAGAACACAAAGCCAGGCTCTGCTCTTTGAGGTAAAGGAGATCTTCAAGGGAAGTCAC 724
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QY 712 CTTT---CCTGGTACCAAGGGCAGTGTTAGCATCATGGATGGATCC--GACGAAGGCAT 766
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Db 725 CTTTCCCTGGGTACCAAGGGCAGTGTTAGCATCATGGATGGATCCCGAAGGGGCAT 784
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QY 767 ATTAGCTTGGTTACTG 783
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Db 785 ATTAGCTGGGTACTG 801
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RESULT 14
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DEFINITION 602684782P1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:4817229 5',
mRNA sequence.
ACCESSION BG702864
VERSION BG702864.1 GI:13974632
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 878)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: Miklos Palokovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM10717 row: c column: 22
High quality sequence stop: 767.

FEATURES
source
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/note="Organ: brain; Vector: pBluescriptR (modified
pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI (gtcgag
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Institutes of Health). Note: this is a NIH_MGC Library."

BASE COUNT 237 a 190 c 240 g 211 t
ORIGIN

